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- New embodiments of the HIV principal neutralizing determinant.
- (a) New amino acid sequences of an envelope fragment of HIV are disclosed, as well as immunological conjugates for immunological purposes, including vaccination against AIDS.

Acquired Immune Deficiency Syndrome (AIDS) is the clinical manifestation of the apparent infection of CD4 helper T-cells and other cell targets by human immunodeficiency virus (HIV), also previously referred to as human T-lymphotropic virus type III (HTLV-III), Lymphoadenopathy-associated virus (LAV), or AIDS-related virus (ARV) (hereinafter collectively "HIV"). AIDS is a transmissible deficiency of cellular immunity characterized by opportunistic infections and certain malignancies. A similar disease, AIDS-related complex (ARC), shares many of the epidemiological features and immune abnormalities with AIDS, and often precedes the clinical manifestations of AIDS.

A vaccine against AIDS and/or ARC is an ideal prophylactic treatment for preventing the delibilitating effects of infection by HIV. Applicants have discovered new immunogens useful for such a vaccine. The immunogens are new principal neutralizing determinants (PNDs) of HIV.

Many of the details of the genetic function and virion structure of HIV have not yet been elucidated. However, certain general features have emerged. An RNA virus with a genome totaling about 9 kilobases (kb), its nucleotide sequence contains seven major open reading frames (ORFs) corresponding to the gag, pol and env, vif, tat, rev, and nef genes. The genes gag, pol and env code respectively for core subunits, viral enzymes such as reverse transcriptase or protease, and outer surface subunits. The gene vif codes for a viral infectivity factor, which is a protein involved with enhancement of cell-to-cell transmission of virions without affecting the budding process. The gene tat codes for a small protein that transactivates the expression of all viral proteins. The gene rev regulates expression of the viral proteins of gag, pol and env genes, possibly by facilitating transport of incompletely spliced RNA. The nef gene codes for a viral protein found in the cell cytoplasm, and it may modulate the host cellular signaling system and serve as a transciptional silencer. Terminal repeats in the nucleotide sequence are common to many retroviruses such as HIV and are required for viral replication and integration into the host chromosome. More recent discussions on the general nature of HIV genomic structure, replication and regulation are found in Ratner, L. et al. "Human T-Lymphotropic Retroviruses," in O'Brien, S.J. (ed.) Genetic Maps 1987 Cold Spring Harbor 1987 pp. 124-129; Franchini, G. et al., Nature 328, 539 (1987); Varmus, H. Genes & Dev 2, 1055 (1988).

Principal neutralizing determinants (PNDs) have been located within a selected, conserved region of the env gene. These PNDs are still undefined. Applicants have discovered and defined new embodiments of PND.

AIDS is a disease of a virus with a unique collection of attributes. HIV itself targets the immune system; it possesses a reverse transcriptase capable of turning out highly mutated progeny; it is sequestered from the immune system and it has a hypervariable surface in the (env) region. See, e.g. Hilleman, M.R., Vaccine 6, 175 (1988); Barnes, D.M., Science 240, 719 (1988). In view of these attributes, it was neither anticipated nor expected that the principal neutralizing determinants of this invention would serve as effective AIDS immunogens.

#### **BRIEF DESCRIPTION OF THE INVENTION**

New principal neutralizing determinants of HIV are disclosed, and are useful as immunogens for AIDS vaccines, particularly in the form of conjugates

#### ABBREVIATIONS AND DEFINITIONS

	AIDS ARC	Acquired immune deficiency syndrome AIDS-related complex
45	conjugation	The process of covalently attaching 2 molecules each containing one or more immunological determinants, e.g., HIV envelope frag-
		ments and Omp
50	conjugate.	Result of conjugation, also known as an antigenic conjugate or immunological conjugate
30	HIV	Generic term for the presumed etiological agent of AIDS and/or ARC, also referred to as strains HTLV-III, LAV, and ARV.
	PND	Principal neutralization determinant of HIV
	Omp	Outer membrane proteosome
55	Recombinant protein	A polypeptide or oligopeptide expressed by foreign DNA in a recombinant eukaryotic or procaryotic expression system.
	Recombinant expression system	A cell containing a foreign DNA expressing a foreign protein or a foreign oligopeptide.

Amino Acids			
Full Name	Three-letter symbol	One-letter symbol	
Alanine	Ala	Α	
Arginine	Arg	R	
Asparagine	Asn	N	
Aspartic acid	Asp	D	
Asn and/or Asp	Asx	В	
Cysteine	Cys	С	
Glutamine	Ğln	Q	
Glutamic acid	Glu	E	
Gln and/or Glu	Glx	Z	
Glycine	Gly	G	
Histidine	His	Н	
Isoleucine	lle	1	
Leucine	Leu	L	
Lysine	Lys	K	
Methionine	Met	M	
Phenylalanine	Phe	F	
Proline	Pro	P	
Serine	Ser	S	
Threonine	Thr	Т	
Tryptophan	Trp	w	
Tyrosine	Tyr	Y	
Valine	Val	V	

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Nucleotides Bases in DNA or RNA	
Name	One-letter symbol
Adenine	Α
Cytosine	С
guamine	G
thymine	Т
uracil	υ

The terms "protein," "peptide," "oligopeptide," and "polypeptide" and their plurals have been used interchangeably to refer to chemical compounds having amino acid sequences of five or more amino acids. "Amino acid" refers to any of the 20 common amino acids for which codons are naturally available, and are listed in the table of amino acids given above.

When any variable (e.g. PND) occurs more than one time in any constituent or in Formula I, its definition on each occurrence is independent of its definition at every other occurrence. Also, combinations of substituents and/or variables are permissible only if such combinations result in stable compounds.

## DETAILED DESCRIPTION OF THE INVENTION

The present invention provides an effective immunogen against AIDS or ARC, and comprises an antigenic conjugate of the formula

(PND)<sub>n</sub>~ (Omp) I,

55 wherein:

PND is the principal neutraliziation determinant of HIV, which is a polypeptide of one or more amino acid sequences;

n = 1-50, wherein n is the number of polypeptides of PND covalently linked to Omp;

indicates covalent linkage;

Omp is outer membrane proteosome of the microorganism Neisseria;

said polypeptide containing in its sequence Gly-X-Gly, wherein X is proline, leucine, alanine, glutamine or serine.

The antigenic conjugates of this invention are prepared by isolating and purifying their component parts PND and Omp, then conjugating PND and Omp together. Subsequent purification of conjugate mixtures may be performed as desired.

The new PND amino acid sequences of this invention include any fragment thereof, provided said fragment is at least five amino acids in length.

Each PND amino acid sequence is determined by DNA sequencing of HIV clones amplified by the polymerase chain reaction.

#### Polymerase Chain Reaction Amplification

Large amounts of DNA coding for PND protein may be obtained using polymerase chain reaction (PCR) amplification techniques as described in Mullis et al., U.S. Patent No. 4,800,159 and other published sources. See also, for example, Innis, M.A. et al. PCR Protocals Academic Press 1990. The extension product of one primer, when hybridized to another primer, becomes a template for the synthesis of another nucleic acid molecule.

The primer template complexes act as substrate for DNA polymerase which, in performing its replication function, extends the primers. The region in common with both primer extensions, upon denaturation, serves as template for a repeated primer extension.

Taq DNA Polymerase catalyzes primer extension in the amplification process. The enzyme is a thermostable DNA polymerase isolated from Thermus aquaticus. Because it stays active through repeated elevations to high denaturation temperatures, it needs to be added only once. Deoxynucleotide triphosphates provide the building blocks for primer extension.

The nucleic acid sequence strands are heated until they separate, in the presence of oligonucleotide primers that bind to their complementary strand at a particular site of the template. This process is continued with a series of heating and cooling cycles, heating to separate strands, and cooling to reanneal and extend the sequences. More and more copies of the strands are generated as the cycle is repeated. Through amplification, the coding domain and any additional primer-encoded information such as restriction sites or translation signals (signal sequences, start codons and/or stop codons) is obtained.PCR protocols are often performed at the 100 µL scale in 0.5 ml microcentrifuge tubes. The PCR sample may be single-or double-stranded DNA or RNA. If the starting material is RNA, reverse transcriptase is used to prepare first strand cDNA prior to PCR. Typically, nanogram amounts of cloned template, up to microgram amounts of genomic DNA, or 20,000 target copies are chosen to start optimization trials.

PCR primers are oligonucleotides, typically 15 to 50 bases long, and are complementary to sequences defining the 5' ends of the complementary template strands. Non-template complementary 5' extensions may be added to primers to allow a variety of useful post amplification operations on the PCR product without significant perturbation of the amplification itself. It is important that the two PCR primers not contain more than two bases complementary with each other, especially at their 3' ends. Internal secondary structure should be avoided in primers.

Because Taq DNA Polymerase has activity in the 37-55°C range, primer extension will occur during the annealing step and the hybrid will be stabilized. The concentrations of the primers are preferably equal in conventional PCR and, typically, are in vast excess of the template to be reproduced.

In one typical PCR protocol, each deoxynucleotide triphosphate concentration is preferably about 200  $\mu$ M. The four dNTP concentrations are preferably above the estimated Km of each dNTP (10-15  $\mu$ M).

Preferably PCR buffer is composed of about 500 mM potassium chloride, 10.0 mM Tris-HCl (pH 8.3 at room temperature), 1.5 mM magnesium chloride, and 0.01% w/v gelatin. In the presence of 0.8 mM total dNTP concentration, a titration series in small increments over the 1.5-to 4-mM range will locate the magnesium concentration producing the highest yield of a specific product. Too little free magnesium will result in no PCR product and too much free magnesium may produce a variety of unwanted products.

Preferably, in a 100-µL reaction volume, 2.0 to 2.5 units of <u>Taq</u> DNA Polymerase are recommended. The enzyme can be added conveniently to a fresh master mix prepared for a number of reactions, thereby avoiding accuracy problems associated with adding individual 0.5-µL enzyme aliquots to each tube. A typical PCR protocol for amplification of the DNA template includes a 1 minute 94°C denaturation step, a 1 minute 37°C primer annealing step, and a 2 minute 72°C primer extension step. This will amplify a 500 base-pair product at least 100,000-fold in 25 cycles.

During DNA denaturation, sufficient time must be allowed for thermal equilibration of the sample. The practical range of effective denaturation temperatures for most samples is 92-95°C, with 94°C being the standard choice.

Primer annealing is usually performed first at 37°C, and the specificity of the product is evaluated. If unwanted bands are observed, the annealing temperature should be raised in subsequent optimization runs. While the primer annealing temperature range is often 37-55°C, it may be raised as high as the extension temperature in some cases. Merging of the primer annealing and primer extension steps results in a two-step PCR process.

Primer extension, in most applications, occurs effectively at a temperature of 72°C and seldom needs optimization. In the two-temperature PCR process the temperature range may be 65-70°C. In situations where enzyme concentration limits amplification in late cycles, the extension is preferably increased linearly with cyclic number. Usually, 25 to 45 cycles are required for extensive amplification (i.e., 1,000,000 fold) of a specific target.

Once the DNA sequence is determined, through conventional and well-known techniques, its amino acid sequence can be deduced by "translating" the DNA sequence. The resulting amino acid sequence having the principal neutralizing determinant of the envelope gene is then employed to synthesize large quantities of PND protein or fragment thereof. Synthesis is performed by organic synthesis or by recombinant expression systems, or both.

# Preparation of Principal Neutralization Determinant

# A. Organic Synthesis of PND:

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Standard and conventional methods exist for rapid and accurate synthesis of long peptides on solidphase supports. Solution-phase synthesis is usually feasible only for selected smaller peptides.

Synthesis on solid-phase supports, or solid-phase synthesis, is most conveniently performed on an automated peptide synthesizer according to e.g., Kent, S. et al., "Modern Methods for the Chemical Synthesis of Biologically Active Peptides," in Alitalo, K. et al., (eds.). Synthetic Peptides in Biology and Medicine, Elsevier 1985, pp. 29-57. Manual solid-phase synthesis may be employed instead, by following the classical Merrifield techniques, as described, for example, in Merrifield, R.B. J. Am. Chem. Soc. 85, 2149 (1963), or known improvements thereof. Solid-phase peptide synthesis may also be performed by the Fmoc method, which employs very dilute base to remove the Fmoc protecting group. Segment synthesis-condensation is a further variant of organic synthesis of peptides as within the scope of the techniques of the present invention.

In organic synthesis of peptides, protected amino acids are condensed to form amide or peptide bonds with the N-terminus of a growing peptide. Condensation is usually performed with the carbodiimide method by reagents such as dicyclohexylcarbodiimide, or N-ethyl, N<sub>1</sub>-(γ-dimethylaminopropyl) carbodiimide. Other methods of forming the amide or peptide bond include, but are not limited to, synthetic routes via an acid chloride, azide, mixed anhydride or activated ester. Common solid-phase supports include polystyrene or polyamide resins.

The selection of protecting groups of amino acid side claims is, in part, dictated by particular coupling conditions, in part by the amino acid and peptide components involved in the reaction. Such amino-protecting groups ordinarily employed include those which are well known in the art, for example, urethane protecting substituents such as benzyloxycarbonyl (carbobenzoxy), p-methoxycarbobenzoxy, p-nitrocarbobenzoxy, t-butyloxycarbonyl, and the like. It is preferred to utilize t-butoxycarbonyl (BOC) for protecting the  $\epsilon$ -amino group, in part because the BOC protecting group is readily removed by relatively mild acids such as trifluoroacetic acid (TFA), or hydrogen chloride in ethyl acetate.

The OH group of Thr and Ser may be protected by the Bzl (benzyl) group and the ε-amino group of Lys may be protected by the isopropoxycarbonyl (IPOC) group or the 2-chlorobenzyloxycarbonyl (2-CI-CBZ) group. Treatment with HF or catalytic hydrogenation are typically employed for removal of IPOC or 2-CI-CBZ.

For preparing cocktails of closely related peptides, see, e.g., Houghton, R.A., Proc. Natl. Acad. Sci. USA 82, 5131 (1985).

# B. Expression of PND in a Recombinant Expression System

It is now a relatively straightforward technology to prepare cells expressing a foreign gene. Such cells act as hosts and include E. coli, B. subtilis, yeasts, fungi, plant cells or animal cells. Expression vectors for

many of these host cells have been isolated and characterized, and are used as starting materials in the construction, through conventional recombinant DNA techniques, of vectors having a foreign DNA insert of interest. Any DNA is foreign if it does not naturally derive from the host cells used to express the DNA insert. The foreign DNA insert may be expressed on extrachromosomal plasmids or after integration in whole or in part in the host cell chromosome(s), or may actually exist in the host cell as a combination of more than one molecular form. The choice of host cell and expression vector for the expression of a desired foreign DNA largely depends on availability of the host cell and how fastidious it is, whether the host cell will support the replication of the expression vector, and other factors readily appreciated by those of ordinary skill in the art.

The technology for recombinant procaryotic expression systems is now old and conventional. The typical host cell is E. coli. The technology is illustrated by treatises such as Wu, R (ed) Meth. Enzymol. 68 - (1979) and Maniatis, T. et. al., Molecular Cloning: A Laboratory Manual Cold Spring Harbor 1982.

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The foreign DNA insert of interest comprises any DNA sequence coding for a PND (or fragment thereof of at least 5 amino acids in length) of the present invention, including any synthetic sequence with this coding capacity or any such cloned sequence or combination thereof. For example, PND peptide coded and expressed by an entirely recombinant DNA sequence is encompassed by this invention.

Vectors useful for constructing eukaryotic expression systems for the production of recombinant PND comprise the DNA sequence for PND, fragment or variant thereof, operatively linked thereto with appropriate transcriptional activation DNA sequences, such as a promoter and/or operator. Other typical features may include appropriate ribosome binding sites, termination codons, enhancers, terminators, or replicon elements. These additional features can be inserted into the vector at the appropriate site or sites by conventional splicing techniques such as restriction endonuclease digestion and ligation.

Yeast expression systems, which are one variety of recombinant eukaryotic expression systems, generally employ Saccharomyces cerevisiae as the species of choice for expressing recombinant proteins. S. cerevisiae and similar yeasts possess well known promoters useful in the construction of yeast expression systems, including but not limited to GAP491, GAL10, ADH2, and alpha mating factor.

Yeast vectors useful for constructing recombinant yeast expression systems for expressing PND include, but are not limited to, shuttle vectors, cosmid plasmids, chimeric plasmids, and those having sequences derived from 2-micron circle plasmids.

Insertion of the appropriate DNA sequence coding for PND, fragment or variant thereof, into these vectors will, in principle, result in a useful recombinant yeast expression system for PND where the modified vector is inserted into the appropriate host cell, by transformation or other means.

Recombinant mammalian expression systems are another means of producing the recombinant PND for the conjugates of this invention. In general, a host mammalian cell can be any cell that has been efficiently cloned in cell culture. Host mammalian cells useful for the purposes of constructing a recombinant mammalian expression system include, but are not limited to, Vero cells, NIH3T3, GH3, COS, murine C127 or mouse L cells. Mammalian expression vectors can be based on virus vectors, plasmid vectors which may have SV40, BPV or other viral replicons, or vectors without a replicon for animal cells. Detailed discussions on mammalian expression vectors can be found in the treatises of Glover, D.M. (ed.) "DNA Cloning: A Practical Approach," IRL 1985, Vols. I and II.

Recombinant PND may possess additional and desirable structural modifications not shared with the same organically synthesized peptide, such as adenylation, carboxylation, glycosylation, hydroxylation, methylation, phosphorylation or myristoylation. These added features may be chosen or preferred as the case may be, by the appropriate choice of recombinant expression system. On the other hand, recombinant PND may have its sequence extended by the principles and practice of organic synthesis of section A above.

## Conjugation of PND and Omp to Form a Covalent Linkage(s) Yielding Conjugate

Antigenic conjugates of PND and Omp are useful for vaccination against AIDS or ARC. Such conjugates have at least one covalent linkage between the antigen PND and Omp, and typically have more than one PND molecule covalently bound to each Omp molecule.

PND and Omp are prepared separately, then linked by non-specific cross-linking agents, monogeneric spaces or bigeneric spacers. Methods for non-specific cross-linking include, but are not limited to, reaction with glutaraldehyde; reaction with N-ethyl-N'-(3-dimethylaminopropyl) carbodiimide, with or without admixture of a succinylated carrier; periodate oxidation of glycosylated substituents followed by coupling to free amino groups of a protein carrier in the presence of sodium borohydride or sodium cyanoborohydride; diazotization of aromatic amino groups followed by coupling on tyrosine side chain residues of the protein;

reaction with isocyanates; or reaction of mixed anhydrides. See, generally, Briand, J.P. et al. J. Imm. Meth. 78, 59 (1985). These methods of non-specifically cross-linking are conventional and well-known in the typical practice of preparing conjugates for immunological purposes.

In another embodiment of the invention conjugates formed with a monogeneric spacer are prepared. These spacers are bifunctional and require functionalization of only one of the partners of the reaction pair to be conjugated before conjugation takes place.

By way of illustration rather than limitation, an example of a monogeneric spacer involves coupling the polypeptide PND to one end of the bifunctional molecule adipic acid dihydrazide in the presence of carbodiimide. A diacylated hydrazine presumably forms with pendant glutamic or aspartic carboxyl groups of PND. Conjugation then is performed by a second coupling reaction with carrier protein in the presence of carbodiimide. For similar procedures, see for example, Schneerson, R. et al., J. Exp. Med. 152, 361 (1980). Another example of a monogeneric spacer is described in Fujii, N. et al. Int. J. Peptide Protein Res. 26, 121 (1985).

In another embodiment of the invention conjugates of PND and Omp are formed with a bigeneric spacer. These spacers are formed after each partner of the reaction pair to be conjugated, e.g., PND and Omp, is functionalized with a bifunctional spacer. Conjugation occurs when each functionalized partner is reacted with its opposite partner to form a stable covalent bond or bonds. See, for example, Marburg, S. et al., J. Am. Chem. Soc. 108, 5282-5287 (1986) and Marburg, S. et al., U.S. Patent 4,695,624, issued 22 September 1987, each incorporated by reference. Bigeneric spacers are preferred for preparing conjugates in human vaccines since the conjugation reaction is well characterized and easily controlled.

Typical and conventional immunological practice provides for the ready and easy synthesis of antigenic conjugates within the scope of the present invention, including the conjugation of Omp with virtually any desired degree of substitution of virtually any peptide of the Sequence Listing. Heterogeneous products of the conjugation reaction are easily separable if needed by a variety of suitable column chromatography techniques.

### Vaccine Formulation

The form of the immunogen within the vaccine takes various molecular configurations. A single molecular species of the antigenic conjugate (PND)<sub>n</sub>~Omp will often suffice as a useful and suitable antigen for the prevention or treatment of AIDS or ARC. Other antigens in the form of cocktails are also advantageous, and consist of a mixture of conjugates that differ by, for example, the degree of substitution (n) or the amino acid sequence of PND or both.

An immunological vector or adjuvant may be added as an immunological vehicle according to conventional immunological testing or practice.

The conjugates of this invention when used as a vaccine, are to be administered in immunologically effective amounts. Dosages of between 1  $\mu$ g and 500  $\mu$ g of conjugate, and perferably between 50  $\mu$ g and 300  $\mu$ g of conjugate are to be administered to a mammal to induce anti-peptide, anti-HIV, or HIV-neutralizing immune responses. About two weeks after the initial administration, a booster dose may be administered, and then again whenever serum antibody titers diminish. The conjugate should be given intramuscularly at a concentration of between 10  $\mu$ g/ml and 1 mg/ml, and preferably between 50 and 500  $\mu$ g/ml, in a volume sufficient to make up the total required for immunological efficacy.

Adjuvants may or may not be added during the preparation of the vaccines of this invention. Alum is the typical and preferred adjuvant in human vaccines, especially in the form of a thixotropic, viscous, and homogeneous aluminum hydroxide gel. For example, one embodiment of the present invention is the prophylactic vaccination of patients with a suspension of alum adjuvant as vehicle and a cocktail of (PND)<sub>n</sub>-Omp as the selected set of immunogens or antigens.

The vaccines of this invention may be effectively administered, whether at periods of pre-exposure and/or post-exposure, in combination with effective amounts of the AIDS antivirals, immunomodulators, anti-infectives, or vaccines of Table I.

# TABLE I

		ANTI-VIRALS	
5	Drug Name	<u>Manufacturer</u>	<u>Indication</u>
	AL-721	Ethigen	ARC, PGL
		(Los Angeles, CA)	HIV positive, AIDS
10			
	Recombinant Human	Triton Biosciences	AIDS, Kaposi's
	Interferon Beta	(Almeda, CA)	sarcoma, ARC
15			
	Acemannan	Carrington Labs	ARC
		(Irving, TX)	(See also immuno-
			modulators)
20			
	Cytovene	Syntex	sight threateining CMV
	Ganciclovir	(Palo Alto, CA)	peripheral CMV
25			retinitis
	1.4 m	Deigtol Myorg	AIDS, ARC
	d4T	Bristol-Myers	AIDS, AIC
30	Didehydrodeoxy-	(New York, NY)	
	thymidine		
•	dd	Bristol-Myers	AIDS, ARC
35	Dideoxyinosine	(New York, NY)	
	-		
	EL10	Elan Corp, PLC	HIV infection
40		(Gainesville, GA)	(See also immuno-
			modulators)
			Out _alimitia UTV
45	Foscarnet	Astra Pharm.	CMV retinitis, HIV
	Trisodium	Products, Inc.	infection, other CMV
	Phosphonoformate	(Westborough, MA)	infections

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. 5	<pre>Drug Name Dideoxycytidine; ddc</pre>	Manufacturer Hoffman-La Roche (Nutley, NJ)	Indication AIDS, ARC
10	Novapren	Novaferon Labs, Inc. (Akron, OH) Diapren, Inc. (Roseville, MN, marke	
15	Peptide T Octapeptide Sequence	Peninsula Labs (Belmont, CA)	AIDS
20	Retrovir Zidovudine; AZT	Burroughs Wellcome (Rsch. Triangle Park, NC)	Kaposi's sarcoma,
25			asymptomatic HIV infection, less severe HIV disease, neurological involve-
30			ment, in combination w/other therapies, post-exposure pro-
35			phylaxis in health care workers
40	Rifabutin Ansamycin LM 427	Adria Laboratories (Dublin, OH) Erbamont (Stamford, CT)	ARC .

5	<u>Drug Name</u> Dextran Sulfate	Manufacturer Ueno Fine Chem. Ind. Ltd. (Osaka, Japan)	Indication AIDS, ARC, HIV positive asymptomatic
10	Virazole Ribavirin	Viratek/ICN (Costa Mesa, CA)	asymptomatic HIV positive, LAS, ARC
15	Alpha Interferon	Burroughs Wellcome (Rsch. Triangle Park, NC)	Kaposi's sarcoma, HIV in combination w/Retrovir
20		Immuno-modulators	
25	Drug Name Antibody which neutralizes pH labile alpha aber- rant Interferon in an immuno- adsorption column	Manufacturer Advanced Biotherapy Concepts (Rockville, MD)	Indication AIDS, ARC
35	AS-101	Wyeth-Ayerst Labs. (Philadelphia, PA)	AIDS
40	Bropirimine	Upjohn (Kalamazoo, MI)	advanced AIDS
	Acemannan	Carrington Labs, Inc. (Irving, TX)	AIDS, ARC (See also anti-

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virals)

	Drug Name CL246,738	Manufacturer American Cyanamid (Pearl River, NY)	Indication AIDS, Kaposi's sarcoma
5		Lederle Labs (Wayne, NJ)	
10	EL10	Elan Corp, PLC	HIV infection
		(Gainesville, GA)	(See also anti-
			virals)
15	Gamma Interferon	Genentech	ARC, in combination
		(S. San Francisco,	w/TNF (tumor necrosis
		CA)	factor)
20			
	Granulocyte	Genetics Institute	AIDS
	Macrophage Colony	(Cambridge, MA)	
25	Stimulating	Sandoz	
	Factor	(East Hanover, NJ)	
	Granulocyte	Hoeschst-Roussel	AIDS
30	Macrophage Colony	(Somerville, NJ)	
	Stimulating	Immunex	
	Factor	(Seattle, WA)	
35			
	Granulocyte	Schering-Plough	AIDS
	Macrophage Colony	(Madison, NJ)	
40	Stimulating Factor		AIDS, in combination
			w/Retrovir
	HIV Core Particle	Rorer	seropositive HIV
45	Immunostimulant	(Ft. Washington, PA)	

	Drug Name	Manufacturer	<u>Indication</u>	
	IL-2	Cetus	AIDS, in combaintion	
5	Interleukin-2	(Emerycille, CA)	w/Retrovir	
	IL-2	Hoffman-La Roche	AIDS, ARC, HIV, in	
10	Interleukin-2	(Nutley, NJ)	combination w/Retrovir	
	Immune Globulin	Cutter Biological	pediatric AIDS, in	
15	Intravenous	(Berkeley, CA)	combination	
	(human)		w/Retrovir	
20	IMREG-1	Imreg	AIDS, Kaposi's	
20		(New Orleans, LA)	sarcoma, ARC, PGL	
	IMREG-2	Imreg	AIDS, Kaposi's	
25		(New Orleans, LA)	sarcoma, ARC, PGL	
	Imuthiol Diethyl	Merieux Institute	AIDS, ARC	
30	Dithio Carbamate	(Miami, FL)	4	
	INTRON A	Schering Plough	Kaposi's sarcoma	
	Alpha-2	(Madison, NJ)	w/Retrovir: AIDS	
. 35	Interferon			
٠	Methionine-	TNI Pharmaceutical	AIDS, ARC	
40	Enkephalin	(Chicago, IL)	•	
	MTP-PE	Ciba-Geigy Corp.	Kaposi's sarcoma	
	Muramy1-	(Summit, NJ)		
	Tripeptide			

5	Drug Name Granulocyte Colony Stimulating Factor	Manufacturer Amgen (Thousand Oaks, CA)	Indication AIDS, in combination w/Retrovir
10	rCD4 Recombinant Soluble Human CD4	Genentech (S. San Francisco, CA)	AIDS, ARC
15	Recombinant Soluble Human CD4	Biogen (Cambridge, MA)	AIDS, ARC
20	Roferon-A Interferon Alfa 2a	Hoffman-La Roche (Nutley, NJ)	Kaposi's sarcoma AIDS, ARC, in combination w/Retrovir
30	SK&F106528 Soluble T4	Smith, Kline & French Laboratories (Philadelphia, PA)	HIV infection
35	Thymopentin	Immunobiology Research Institute (Annandale, NJ)	HIV infection
40	Tumor Necrosis Factor; TNF	Genentech (S. San Francisco, CA)	ARC, in combina- tion w/gamma Interferon

# Anti-Infectives

5	Drug Name Clindamycin with Primaquine	Manufacturer Upjohn (Kalamazoo, MI)	Indication PCP
10	Diflucan Fluconazole	Pfizer (New York, NY)	cryptococcal meningitis, candidiasis
15	Pastille Nystatin Pastille	Squibb Corp. (Princeton, NJ)	prevention of oral candidiasis
20	Ornidyl Eflornithine	Merrell Dow (Cincinnati, OH)	PCP
25	Pentamidine Isethionate (IM & IV)	LyphoMed (Rosemont, IL)	PCP treatment
30	Piritrexim	Burroughs Wellcome (Rsch. Triangle Park, NC)	PCP treatment
35	Pentamidine isethionate for inhalation	Fisons Corporation (Bedford, MA)	PCP prophylaxis
45	Spiramycin	Phone-Poulenc Pharmaceuticals (Princeton, NJ)	cryptosporidial diarrhea

5	Drug Name Intraconazole- R51211	Manufacturer Janssen Pharm. (Piscataway, NJ)	Indication histoplasmosis; cryptococcal meningitis
10	Trimetrexate	Warner-Lambert	PCP
		<u>Other</u>	
15 20	Drug Name Recombinant Human Erythropoietin	Manufacturer Ortho Pharm. Corp. (Raritan, NJ)	Indication severe anemia assoc. and Retrovir therapy
25	Megestrol Acetate	Bristol-Myers (New York, NY)	treatment of anorexia assoc. w/AIDS
30	Total Enteral	Norwich Eaton Pharmaceuticals (Norwich, NY)	diarrhea and malabsorption related

It will be understood that the scope of combinations of the antigenic conjugates of this invention with AIDS antivirals, immunomodulators, anti-infectives or vaccines is not limited to the list in the above Table, but includes in principle any combination with any pharmaceutical composition useful for the treatment of AIDS. The antigenic conjugates as AIDS or HIV vaccines of this invention include vaccines to be used preor post-exposure to prevent or treat HIV infection or disease, and are capable of producing an immune response specific for the immunogen.

#### **EXAMPLE 1**

Isolation of Genomic DNA from Frozen (-20°C) Pellets of Peripheral Blood Lymphocytes

Each DNA was prepared respecting the principle that preparation and storage of high molecular weight DNA be segregated from all polymerase chain reaction (PCR) amplification experiments.

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5	Reagents P-K Buffer 10 mM Tris 400 mM NaC1 2 mM EDTA	рН 7.4	Prepare using sterile H <sub>2</sub> 0 in plastic labware. Sterile filter through a 0.45 µm filter device and aliquot 10 ml into 15 ml conical tubes. Store at -20°C.
15	Proteinase K	1.0mg/m1	Dissolve the contents of a bottle in sterile H <sub>2</sub> O to a final conc. of 1.0 mg/ml. Aliquot 0.3-0.5 ml into freezer tubes. Store at -20°C.
25	SDS 10%		Prepare using sterile H <sub>2</sub> O in plastic labware. Sterile filter through a 0.45 µm filter device and aliquot 2.0 ml into Nalgene freezer tubes. Store at -20°C.
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Phenol:Chloroform 50:50 Prepare and aliquot 8.0 ml into 15 ml conical tubes and store at -20°C in the dark.

RNase A 1.0 mg/ml

Dissolve the contents of a bottle in sterile H<sub>2</sub>O to a final conc. of 1.0 mg/ml. Aliquot 0.3-0.5 ml into freezer tubes. at -20°C.

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95% and 70% EtOH

Store at -20°C.

Dilution Buffer 20 10 mM Tris 25 mM NaCl pH 8.0

0.1 mM EDTA

Prepare using sterile H<sub>2</sub>0 in plastic labware. Sterile filter through a 0.45 µm filter device and aliquot 10 ml in 15 ml conical tubes. Store at 4°C.

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- 1) Suspend cell pellets of co-cultivated patient peripheral blood lymphocytes in 0.5 ml of P-K Buffer taking care to break up pellet completely.
- 2) Adjust sample to 100 µg/ml Proteinase K with 1.0 mg/ml stock. Mix well.
- 3) Adjust sample to 0.5% SDS with 10% stock. Mix well and incubate at 50°C for 16-24 hours.
- 4) Extract sample with an equal volume of Phenol: Chloroform for 10 minutes @ 21-25° C.
- 5) Split phases by centrifugation @ 2K for 5 minutes.
- 6) Remove aqueous and re-extract with an equal vol. of CHCl3 for 2-5 minutes @ 21-25 °C. Split phases as before. 35
  - 7) Repeat Step 6.
  - 8) Adjust aqueous to 100 μg/ml RNase A with 1.0 mg/ml stock and incubate @ 37 °C for 90 minutes.
  - 9) Repeat Steps 4, 5, 6, and 7.
  - 10) Precipitate DNA with the addition of 2.5 vol of cold 95% EtOH.
- 11) Collect DNA for 30 minutes at 10,000 RPM's at 4°C. 40
  - 12) Remove EtOH and wash pellet once with 70% EtOH. Spin for 2 minutes as 10,000 RPM's.
  - 13) Remove EtOH and dissolve the pellet in  $300\lambda$  of dilution buffer.

#### **EXAMPLE 2**

PCR Amplification of Genomic DNA from HIV Isolates

Genomic DNA was amplified by the polymerase chain reaction according to Scharf, S.J. et al. Science 233, 1076 (1986). A heat resistant T. aquaticus DNA polymerase was employed to enhance stability during thermal cycling. See, e.g., Saiki, R. K. et al. Science 239, 487 (1988). Excess primer for each strand was used. The primers were

RP.Hpa having the sequence

5'-P-TCT-GTT-AAC-TTC-ACA-GAC-AAT-GCT-AAA-ACC-ATA-ATA-GTA-CAG-CTG-3'; and RP.Cla having the sequence

5'-P-GCA-ATC-GAT-CTG-TTT-TAA-AGT-GTT-ATT-CCA-TTT-TGC-3'

The 5' phosphate was added by chemical methods, according to Horn, T. et al., Tetrahedron Letters 27, 4705 (1986).

#### **EXAMPLE 3**

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#### Filtration of PCR Amplified Sequences

#### General Considerations:

This filtration step removes free nucleotides and low molecular weight oligonucleotide contaminants which inhibit ligation, according to Sharf, et al. Science, 233, 1076 (1986).

- 1) Dilute up to 100\(\lambda\) of sample (1-2 \(\mu\g\) DNA/ml) of Example 2 to 400\(\lambda\) with "buffer" (10 mM Tris HCl, 25 mM NaCl, 0.1 mM EDTA, all buffered to pH8) and spin in a microcentrifuge for 5 minutes at RT.
- N.B. No more than 4 samples can be placed in same rotors at one time. Be sure that the cap of the tube is completely closed or some volume may spray out of the unit. If using a non-dedicated microcentrifuge, spin sample at 2000 x g.
- 2) Remove insert and place in a clean 1.5 ml plastic tube containing a polysulfone filter with a 100,000 dalton molecular weight cut off. Redilute sample to 400\lambda with buffer and spin as before.
- 3) Repeat Step 2.
- 4a) For Cloning purposes:

Remove sample and rinse membrane gently with 10-20 $\lambda$  of buffer. Combine the sample and rinse and adjust back to the original volume. Check on agarose gel for yield and purity.

4b) For Reamplification purposes:

Remove sample carefully measuring volume. Rinse the membrane gently with additional buffer as above. Adjust back to the original volume ( $100\lambda$ ) and use  $5\lambda$  of the sample for reamplification.

#### **EXAMPLE 4**

Ligation and Cloning of PCR Amplified Sequences

#### Reagents

pUC13 SmaI/Bap

A cloning vector commercially prepared by Pharmacia, dissolved in 10 mM Tris pH8.0, aliquoted and stored at -20°C. Its

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sequence and preparation are described in Vieira, J. et al., Gene 19, 259 (1982), incorporated by reference for these purposes.

5X ligation buffer 250 mM Tris pH7.8 50 mM MgCl<sub>2</sub> prepared from stocks aliquoted and stored at -20°C.

30 mm mgc1<sub>2</sub>

100 mM DTT

5.5 mM ATP

250 mg/ml BSA

20 T<sub>4</sub> DNA Ligase

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New England Biolabs

SOC media

# Final Concentration

30 Bactotryptone 2%
Yeast Extract 0.5%
NaC1 10 mM

KC1 2.5 mM

MgCl<sub>2</sub>, MgSO<sub>4</sub> 20 mM (10 mM each)
Glucose 20 mM
Distilled H<sub>2</sub>O ----

- To 97 ml distilled H<sub>2</sub>0, add bacto-tryptone, yeast extract, NaCl and KCl. Stir to dissolve, autoclave, and cool to room temperature. Make medium 20 mM in Mg<sup>++</sup> stock with a 2 M Mg<sup>++</sup> (1 M MgCl<sub>2</sub>•6H<sub>2</sub>0 + 1 M MgSO<sub>4</sub>•

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7H<sub>2</sub>O, filtersterilized). Add 2<sup>4</sup>M glucose stock (filtersterilized) to make the medium 20 mM final. Filter the complete medium through a 0.2 µm filter unit. pH should be 7.0 ± 0.1. Filtersterilizing units should be prefiltered with distilled H<sub>2</sub>O before use to remove any toxic material from the filter.

## Luria Bertani Agar + 100 μg/ml

Ampicillin - commercially prepared from REMEL. For composition, see Sambrook, J. et al., Molecular

Cloning 3, A.1 (2nd Ed., 1989)

Xgal 2% in dimethy1-

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formamide - stored at -20°C. Xgal is

5-bromo-4-chloro-3-indolyl

B-D-galactoside.

IPTG 100 mM in  $H_2^0$  - stored at -20°C. IPTG is

isopropyl-thiogalactoside.

- 1). Combine 10λ of filtered PCR amplified DNA (10-20 ng/ml) with 20 ng of pUCl3 Smal/BAP and 100 units of T<sub>4</sub> DNA ligase in a final volume of 20λ.
  - 2). Incubate at 21-25 °C for 3 hours.
  - 3). Transform 100\(\lambda\) of tranformation competent bacteria using 10\(\lambda\) of ligation buffer.
  - 4). Incubate on ice for 30 minutes in sample tubes.

- 5). Heat shock tubes for 45 seconds at 42°C.
- 6). Reincubate on ice for 2 minutes before adding 1.0 ml of SOC media (21-25 °C).
- 7). Incubate 1 hour at 37°C shaking at 225 RPM's.
- 8). Pellet cells in 1.5 ml plastic tubes for 10 seconds at maximum speed.
- 9). Remove the media except about 100λ. Care should be taken removing the media as the pellet is loose
  - 10). Resuspend the cells in the remaining 100 $\lambda$  and spread on an L agar plate containing Ampicillin and onto which 100 $\lambda$  of Xgal and 50 $\lambda$  of IPTG had been previously spread.
  - 11). Invert the incubate at 37° C. Colonies are visible after 12 hours. Blue color indication is clear after 16 hours.

#### **EXAMPLE 5**

Isolation of Plasmid DNA for Subsequent Dideoxy Sequence Analysis

Reagents

MP Buffer 1

20 50 mM Glucose

10 mM EDTA

25 mM Tris pH 8.0

MP Buffer 2 - made fresh for each experiment

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0.2 N NaOH

1% SDS

MP Buffer 3

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Potassium Acetate pH ~5.6

60 ml 5M KOAc

28.5 ml H<sub>2</sub>O

11.5 ml gl. HOAc

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RNase Stock

1.0 mg/ml RNase A dissolved in H2O and boiled

10 minutes

Phenol:Chloroform (50:50)

Phenol is buffer saturated with an equal volume of buffer (50 mM Tris\*HCl, 100 mM NaCl, 1mM EDTA, pH 8.0)

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PEG

13% Poly Ethylene Glycol (PEG-8000)

50 4M NaCl

95% and 70% EtOH

- 1). Three individual colonies from each isolate are selected at random and placed in 10 ml of L Broth. Each are grown overnight in a 50 ml conical tube shaking @ 225-250 RPM's @ 37 ° C.
- 2). Collect 9.5 ml of overnight culture at 1K for 20 minutes.
- 3). Dry pellet well and resuspend by vortexing in 200\(\lambda\) of MP 1. Transfer to a 1.5 ml plastic tube. Incubate 5 minutes @ RT.

- 4). Add 40\(\lambda\) of MP 2 and incubate 5 minutes on ice. Mix by inversion.
- 5). Add 300\(\lambda\) of MP 3 and incubate 5 minutes on ice. Mix by inversion.
- 6). Centrifuge 10,000 Xg for 5 minutes @ 4°C.
- 7). Transfer supernatant to a fresh 1.5 ml tube and add 10λ of a 1.0 μg/ml RNase A stock. Incubate 30 minutes @ 37 °C.
  - 8). Extract with an equal volume (-500\lambda) of buffer saturated phenol:chloroform. Split phases.
  - 9). Transfer aqueous to a fresh tube and precipitate by adding 1.0 ml of cold EtOH. Incubate @ -70 ° C for 30 minutes.
  - 10). Collect at full speed (about 10,000 Xg) for 15 minutes @ 4°C.
  - 11). Remove EtOH and wash with 1.0 ml cold 70% EtOH. Respin for 2 minutes.
  - 12). Remove EtOH and drain tube well. Dry pellet by inversion and then redissolve in  $80\lambda\ H_2O$ .
  - 13). Adjust sample with 20\(\lambda\) 4M NaCl and 100\(\lambda\) PEG. Incubate 30 minutes on ice.
  - 14). Centrifuge at full speed (about 10,000 Xg) for 15 minutes @ 4 ° C.
  - 15). Remove supernatant and wash pellet with 1.0 ml cold 70% EtOH. Respin for 2 minutes.
- 16). Remove EtOH and drain tube well. Dry pellet in speed vac. and then redissolve in 20λ H<sub>2</sub>O.

#### **EXAMPLE 6**

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### **DETERMINATION OF THE DNA SEQUENCE**

Sequencing was performed by the method of Tabor, S. et al., Proc. Nat. Acad. Sci., 84, 4767 (1987). Sequencing gels were read and checked with a scanner. Amino acid sequences were deduced from DNA.

#### **EXAMPLE 7**

Preparation of Synthetic Peptides

A. The oligopeptide EE15-1 of the sequence:

1 5 10 15

Cys Thr Arg Pro Ser Asn Asn Thr Arg Arg Gly Ile His Ile Gly TGT ACA AGA CCC AGC AAC AAT ACA AGA AGA GGT ATA CAT ATA GGA

20 25 30

Pro Gly Arg Ala Leu Tyr Thr Thr Gly Glu Ile Thr Gly Asp Ile CCA GGG AGA GCA CTT TAT ACA ACA GGA GAA ATA ACA GGA GAT ATA

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Arg Arg Ala Tyr Cys

AGA CGA GCA TAT TGT

is synthesized by conventional solid-phase techniques on an automated peptide synthesizer, according to Kent, S. et al., "Modern Methods for the Chemical Synthesis of Biologically Active Peptides," in Alitalo, K. et al.(eds.), Synthetic Peptides in Biology and Medicine, Elsevier 1985, pp. 29-57.

- B. Each of the peptides of the Sequence Listing is prepared by the same method.
- C. Oligopeptide EE15-1 was prepared in a recombinant expression system in E. coli according to the methods of Sambrook, J. et al., Molecular Cloning 3, 17.3 et seq. Cold Spring Harbor 2nd Ed. 1988.

Every other peptide of the Sequence Listing is also prepared in a recombinant expression system in E. coli.

## EXAMPLE 8

## Extraction and Purification of Omp

#### A. First Method

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All materials, reagents and equipment were sterilized by filtration, steam autoclave or ethylene oxide, as appropriate; asceptic technique was used throughout.

A 300 gm (wet weight) aliquot of 0.5% phenol inactivated cell paste of Meningococcal group B11 was suspended in 1200 mls of distilled water than suspended by stirring magnetically for 20 minutes at room temperature. The suspended cells were pelleted at 20,000 xg for 45 minutes at 5°C.

For extraction, the washed cells were suspended in 1500 mls 0.1 M Tris, 0.01 M EDTA Buffer pH 8.5 with 0.5% sodium deoxychloate (TED Buffer) and homogenized with a 500 ml Sorvall omnimixer at setting 3 for 60 seconds. The resulting suspension was transferred to ten Erlenmeyer flasks (500 ml) for extraction in a shaking water bath for 15 minutes at 56°C. The extract was centrifuged at 20,000 x g for 90 minutes at 5°C and the viscous supernatant fluid was decanted (volume = 1500 mls). The decanted fluid was very turbid and was recentrifuged to clarify further at 20,000 x g for 90 minutes at 5°C. The twice spun supernatant fluid was stored at 5°C. The extracted cell pellets were resuspended in 1500 mls TED Buffer. The suspension was extracted for 15 minutes at 56°C and recentrifuged at 20,000 x g for 90 minutes. The supernatant fluids which contained purified Omp were decanted (volume = 1500 mls) and stored at 5°C.

## B. Second Method

All material, reagents, equipment and filters were sterilized by heat, filtration or ethylene oxide. One exception was the K-2 ultracentrifuge which was sanitized with a 0.5% formalin solution. Laminar flow canopies provided sterility protection during equipment connections. Aseptic techniques were followed throughout the entire operations. Overnight storage of the protein was at 2-8 °C between steps. A 0.2 micron sterile filtration was conducted just before the final diafiltration to ensure product sterility.

Two 600-liter batches of Neisseria meningitidis were fermented and killed with 0.5% phenol, then concentrated to roughly 25 liters using two 10 ft<sup>2</sup> 0.2 micron polypropylene cross-flow filtration membranes. The concentrated broth then was diafiltered with 125 liters of cell wash buffer (0.11 M Sodium Chloride, 17.6 mM Sodium Phosphate Diabasic, 23.3 mM Ammonium Chloride, 1.34 mM Potassium Chloride, adjusted to pH 7 with 85% Phorphoric Acid followed by 2.03 mM Magnesium Sulfate Heptahydrate).

For extraction, an equal volume of 2X-TED buffer (0.2M Tris, 0. 02M EDTA adjusted to pH 8.5 with concentrated HCl followed with the addition of 1.0% sodium deoxycholate) was added to the cell slurry. The resulting slurry was heated to  $56 \pm 3$  °C and maintained at this temperature for 30 minutes to complete the extraction of Omp from the cells.

For further purification, the extracted cell slurry was centrifuged at 30,000 x g (18,000 rpm) in a "one-pass" flow mode in a K-ultracentrifuge, and the supernatant stream was collected. The low-speed supernatant was concentrated to 10 liters on two 0.1-micron polysulfone autoclavable hollow-fiber membranes and collected in an 18 liter sterile bottle. The filtration equipment was given two 4-liter rinses with TED buffer (0.1M Tris, 0.01M EDTA, adjusted to pH 8.5 with concentrated HCI, followed with the addition of sodium deoxycholate to 0.5%) which was combined with the retentate. The retentate was subdivided into two or three equal parts. Each part was centrifuged at 80,000 x g (35,000 rpm) for 30 mintues. The Omp protein was pelleted, and the majority of soluble proteins, nucleic acids and endotoxins remained in the supernatant. The supernatant was discarded. The pelleted protein was resuspended by recirculating 55 ± 5°C TED buffer through the rotor. The first high-speed resuspensions were combined and subjected to a second low-speed spin. The second low-speed spin ensured that residual cell debris was removed from the product stream. The second low speed supernatant was subdivided into two or three equal parts. Each fraction was given two consecutive high-speed spins. All high-speed spins were operated under the same conditions and each further purified the Omp protein.

For sterile filtration and final diafiltration, the third high-speed resuspensions were diluted with an equal volume of TED buffer and filtered through a 0.2 micron cellulose acetate filter. When all fractions were permeated, an 8 L TED buffer rinse was used to flush the filtration system. The permeate and rinse were combined and concentrated to 3 liters on a 0.1 micron polysulfone autoclavable hollow fiber membrane. The material then was diafiltered with 15 liters of sterile pyrogen free water. The retentate was collected in a 4-liter bottle along with a 1-L rinse to give the final product. The final aqueous suspension was stored at 2-8 °C, as purified Omp.

#### C. Third Method

Omp is purified from 0.2 M LiCl-0.1M Na Acetate, pH 5.8, extracts by ultracentrifugation, by the method of C.E. Frasch et al. J. Exp. Med. 140, 87-104 (1974), herein incorporated by reference.

#### **EXAMPLE 9**

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# A. Preparation of (EE15-1 Peptide)-Omp conjugate ("EE15-1-Omp" conjugate)

N-acetylhomocystaminylated outer membrane protein (Omp) of N. meningitidis from 59 mg of Omp (purified by Method B of Example 2) is prepared by the centrifugation method described in Marburg, S. et al., J. Am. Chem. Soc. 108:5282 (1986). This material (about 50 mg) is reacted at pH 8 (6.5 mL 0.1M PO₄ buffer) with 20 mg of N-Ω-bromoacetylated EE15-1 (lyophilized) under N₂ for 18 hours at room temperature.

The reaction mixture is diluted to 10 mL with  $H_2O$  and centrifuged for 2h, at 4  $^{\circ}$  C and 43,000 rpm. The supernatant is removed, and the pellet resuspended, using a Dounce tissue homogenizer, in 10 mL of  $H_2O$ . This suspension is recentrifuged (as above) and the pellet resuspended in 9.5 mL of  $H_2O$ . A low speed spin for 1 minute in a clinical centrifuge removes a flocculent insoluble material if any. The degree of substitution can be determined and calculated by a variety of methods.

## B. Preparation of Other Peptide Conjugates

By the method of Example 9A the following peptide-Omp conjugates are obtained:

(EE15-1)5-Omp,

(EE164-3)4-Omp,

(EE244-1)6-Omp,

(EE310-2)<sub>8</sub>-Omp,

(EE311-1)10-Omp,

(LEST 1-1), 0 Omp

(EE359-2)<sub>6.5</sub>-Omp,

(EE360-1)3.3-Omp, and

(EE543-1)<sub>4.0</sub>-Omp.

#### O EXAMPLE 10

Protocol for Inoculation of Animals with the (EE15-1)<sub>5</sub>-Omp Conjugate (hereinafter "EE-15-1-Omp" conjugate)

Alum is used as an adjuvant during the inoculation series. The inoculum is prepared by dissolving the EE15-1-Omp conjugate in physiologic saline at a final conjugate concentration of 100 μg/ml. Preformed alum (aluminum hydroxide gel) is added to the solution to a final level of 500 μg/ml aluminum. The conjugate is allowed to adsorb onto the alum gel for two hours at room temperature. Following adsorption, the gel with the conjugate is washed twice with physiologic saline and resuspended in the saline to a protein concentration of about 100 μg/ml.

African green monkeys are individually inoculated with four 100 mcg doses of the EE15-1-Omp conjugate adsorbed onto alum. Each dose is injected intramuscularly. The doses are delivered one or five months apart (week 0, 4, 8 and 28). The animals are bled at intervals of two or four weeks. Serum samples are prepared from each bleed to assay for the development of specific antibodies as described in the subsequent examples.

## **EXAMPLE 11**

## Analysis of Sera for Anti-Peptide IgG Antibodies

Each serum sample is analyzed by enzyme-linked immunoadsorbent assay (ELISA). Polystyrene microtiter plates are coated with 0.5 µg per well of the synthetic peptide (not conjugated to Omp) in phosphate-buffered physiological saline (PBS) at 4 °C. Each well is then washed with PBS containing 0.05% TWEEN-20 (PBS-T). Test serum, diluted serially in PBS-T, is added to the peptide-containing wells and allowed to react with the adsorbed peptide for one hour at 36 °C. After washing with PBS-T, alkaline phosphatase-conjugated goat anti-human lgG is added to the test wells and is allowed to react for one hour at 36 °C. The wells are then washed extensively in PBS-T. Each well receives 0.1% p-nitrophenyl phosphate in 10% diethanolamine, pH 9.8, containing 0.5 mM MgCl<sub>2</sub>6H<sub>2</sub>0. The ensuing reaction is allowed

to proceed at room temperature for 30 minutes, at which time it is terminated by the addition of 3.0 N NaOH.

The greater the interaction of antibodies in the test serum with the peptide substrate, the greater is the amount of alkaline phosphatase bound onto the well. The phosphatase enzyme mediates the breakdown of p-nitrophenyl phosphate into a molecular substance which absorbs light at a wavelength of 405 nm. Hence, there exists a direct relationship between the absorbance at 405 nm of light at the end of the ELISA reaction and the amount of peptide-bound antibody.

Titers of anti-(EE15-1-Omp) antibody are thus readily determined.

#### EXAMPLE 12

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# Analysis of Sera for Activity which Specifically Neutralizes HIV Infectivity

Virus-neutralizing activity is determined with an assay described by Robertson et al., J. Virol. Methods 20: 195-202 (1988). The assay measures specific HIV-neutralizing activity in test serum. The assay is based on the observation that MT-4 cells, a human T-lymphoid cell line, are readily susceptible to infection with HIV and, after a period of virus replication, are killed as a result of the infection.

The test serum is treated at 56°C for 60 minutes prior to the assay. This treatment is required to eliminate non-specific inhibitors of HIV replication. Heat treated serum, serially diluted in RPMI-1640 cell culture medium, is mixed with a standard infection dose of HIV. The dose is determined prior to the assay as containing the smallest quantity of virus required to kill all the MT-4 cells in the assay culture after a period of 7 days. The serum-virus mixture is allowed to interact for one hour at 37°C. It then is added to 1.0 x 10<sup>5</sup> MT-4 cells suspended in RPMI-1640 growth medium supplemented with 10% fetal bovine serum. The cultures are incubated at 37°C in a 5% CO<sub>2</sub> atmosphere for 7 days.

At the end of the incubation period, a metabolic dye, DTT, is added to each culture. This dye is yellow in color upon visual inspection. In the presence of live cells, the dye is metabolically processed to a molecular species which yields a blue visual color. Neutralized HIV cannot replicate in the target MT-4 cells and therefore does not kill the cells. Hence, positive neutralization is assessed by the development of blue color following addition of the metabolic dye.

All the monkeys inoculated with the EE15-1-Omp conjugate are bled for specific HIV infectivity-neutralizing activity. Further follow-up evaluation of the same monkeys is also performed. Booster shots are also administered to ascertain renewed neutralizing titer.

While the foregoing specification teaches the principles of the present invention, with examples provided for the purpose of illustration, it will be understood that the practice of the invention encompasses all of the usual variations, adaptations, modifications, deletions or additions of procedures and protocols described herein, as come within the scope of the following claims and its equivalents.

	SEQUENCE LISTING
	(1) GENERAL INFORMATION:
	(i) APPLICANT: J.A. LEWIS ET AL.
5	(ii) TITLE OF INVENTION: NEW EMBODIMENTS OF THE
	HIV PRINCIPAL NEUTRALIZING DETERMINANT
	(iii)CORRESPONDENCE ADDRESS: MERCK & CO., INC.
	(A) STREET: P.O. BOX 2000, EAST LINCOLN AVE.
	(B) CITY: RAHWAY
10	(C) STATE: NEW JERSEY
	(D) COUNTRY: USA
	(E) ZIP: 07065
	(iv) COMPUTER READABLE FORM:
	(A) MEDIUM TYPE: Diskette, 5.25 in., 360 Kb storage
15	(B) COMPUTER: Wang PC 381
	(C) OPERATING SYSTEM: MS-DOS 3.30.10
	(D) SOFTWARE: Microsoft WORD 5.0
	(v) CURRENT APPLICATION DATA:
	(A) APPLICATION NUMBER: NA
20	(B) FILING DATE: NA
	(C) CLASSIFICATION: NA
	(vi) PRIOR APPLICATION DATA: NONE
	(A) DOCUMENT NUMBER:
	(B) COUNTRY:
25	(C) FILING DATE:
	(D) PUBLICATION DATE:
	(vii) ATTORNEY/AGENT INFORMATION:
	(A) NAME: R.D. MEREDITH
	(B) REGISTRATION NUMBER: 30,777
30	(C) REFERENCE/DOCKET NUMBER: 18114Y
	(viii) TELECOMMUNICATION INFORMATION:
	(A) TELEPHONE: 201-594-4678
	(B) TELEFAX: 201-594-4720
	(C) TELEX:
35	(ix) PUBLICATION STATUS: NOT KNOWN
	(A) AUTHORS:
	(B) TITLE:
	(C) JOURNAL:
	(D) VOLUME:
40	(E) ISSUE:
	(F) PAGES:
	(G) DATE:
	(H) RELEVANT RESIDUES:
	(1) START:
45	(2) END:
	(3) BASE PAIRS:
	(4) AMINO ACIDS:

5	(2) INFORMATION FOR SEQ ID NO: EE15-1  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 105  (B) TYPE: Nucleic Acid  (C) STRANDEDNESS: Single  (D) TOPOLOGY: Linear  (ii) KIND:cDNA to genomic RNA  (ii) KIND (if peptide or protein):  (A) SEQUENCE ASSEMBLY METHOD: Overlap  (B) FRACMENT TYPE: Internal Fragment
	(C) HYPOTHETICAL: (iii) ORIGINAL SOURCE: HIV (E) INDIVIDUAL ISOLATE:
15	<ul> <li>(iv) IMMEDIATE SOURCE:</li> <li>(C) CLONE:</li> <li>(v) POSITION IN GENOME: Within Env Gene</li> <li>(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant</li> </ul>
20	(viii) SEQUENCE DESCRIPTION:
	SEQ ID NO: EE15-1
25	
	1 5 10 15
	Cys Thr Arg Pro Ser Asn Asn Thr Arg Arg Gly Ile His Ile Gly TGT ACA AGA CCC AGC AAC AAT ACA AGA AGA GGT ATA CAT ATA GGA
	TOT AUM NUM OOU AND
30	
	20 25 30 Pro Gly Arg Ala Leu Tyr Thr Thr Gly Glu Ile Thr Gly Asp Ile
	CCA GGG AGA GCA CTT TAT ACA ACA GGA GAA ATA ACA GGA GAT ATA
35	
	35
,	Arg Arg Ala Tyr Cys
	AGA CGA GCA TAT TGT
40	
<b>4</b> 5	(2) INFORMATION FOR SEQ ID NO: EE15-2 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 (B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single (D) TOPOLOGY: Linear (ii) KIND:cDNA to genomic RNA

		(ii) KIND (if peptide or protein):  (A) SEQUENCE ASSEMBLY METHOD: Overlap  (B) FRACMENT TYPE: Internal Fragment  (C) HYPOTHETICAL:	
5		(iii) ORIGINAL SOURCE: HIV	
		(E) INDIVIDUAL ISOLATE:  (iv) IMMEDIATE SOURCE:  (C) CLONE:	
		(v) POSITION IN GENOME: Within Env Gene	
10		(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigeni determinant	
		(viii) SEQUENCE DESCRIPTION:	
15	SEQ	ID NO: EE15-2	
	1	5 10 15	
	Cys	Thr Arg Pro Ser Asn Asn Thr Arg Arg Ser Ile Pro Ile Gly	
20	TGT	ACA AGG CCC AGC AAC AAT ACA AGA AGA AGT ATA CCT ATA GGA	
20		,	
		20 25 30	
	Pro	Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile	
25	CCA	GGG AGA GCC TIT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA	
e.J			
		35	
	_	Gln Ala His Cys	
30	AGA	CAA GCA CAT TGT	
	(2)	INFORMATION FOR SEQ ID NO: EE15-3 (i) SEQUENCE CHARACTERISTICS:	
35		(A) LENGTH: 105	
33		(B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single	
		(D) TOPOLOGY: Linear	
		(ii) KIND: cDNA to genomic RNA	
		(ii) KIND (if peptide or protein):	
40		(A) SEQUENCE ASSEMBLY METHOD: Overlap	
		(B) FRACMENT TYPE: Internal Fragment (C) HYPOTHETICAL:	
		(iii) ORIGINAL SOURCE: HIV	
		(E) INDIVIDUAL ISOLATE:	
45		(iv) IMMEDIATE SOURCE:	
		(C) CLONE:	

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5		(vi	11)		EQUEN		DESC	RIPT	ION:	SEQ	ID I	NO: .	_				
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	_	Gln CAA			-					÷							
25	(2)		INF	ORMA:	CION	FOR	SEQ	ID 1	NO:	EEE3	7–1						
			(i)		SEQU (A) (B) (C)	J <b>EN</b> CI	LEN!	ARAC GTH: E: : ANDE	10: Nuc1:	5 eic <i>l</i>	Acid						
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			(iv	)	(E) IMME (C)	DIA:		IVID OURC: NE:		19014	AIE:						
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SEQ ID NO: EEE37-1 10 5 Cys Thr Arg Pro Asn Asn Thr Arg Lys Arg Ile Thr MET Gly TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGG ATA ACT ATG GGA 30 25 20 Pro Gly Arg Val Phe Tyr Thr Thr Gly Gly Ile Ile Gly Asn Ile 10 CCA GGG AGA GTA TIT TAT ACA ACA GGA GGA ATA ATA GGA AAT ATA 35 15 Arg Arg Ala His Cys AGA CGA GCA CAT TGT INFORMATION FOR SEQ ID NO: EEE37-2 (2) 20 SEQUENCE CHARACTERISTICS: (i) (A) LENGTH: 105 TYPE: Nucleic Acid (B) STRANDEDNESS: Single (C) TOPOLOGY: Linear (D) KIND: cDNA to genomic RNA (ii) KIND (if peptide or protein): (ii) SEQUENCE ASSEMBLY METHOD: Overlap (A) FRAGMENT TYPE: Internal Fragment (B) HYPOTHETICAL: (C) 30 ORIGINAL SOURCE: HIV (iii) INDIVIDUAL ISOLATE: (E) IMMEDIATE SOURCE: (iv) CLONE: (C) POSITION IN GENOME: Within Env Gene (v) PROPERTIES OF SEQUENCE: Expresses conserved antigenic (vi) determinant SEQUENCE DESCRIPTION: (viii) SEQ ID NO: BEE37-2

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Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Asn Ile Gly TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA AAT ATA GGA

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	Pro	G1 y	Arg	Ala	Phe	Tyr	Thr	Thr	G1y	G1u	Ile	Ile	G1y	Asp	Ile	
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	Pro	Gly	Pro	Gly	Arg	ALA	rne	Tyr	Inr	Inr	GIA	GIU	116	GLY	ASP	
	CCA	GGA	CCA	GGG	AGA	GUA	TIT	TAT	AUA	ACA	GGA	GAA	AIA	GGA	GAI	
45					26											
-	T1 -	A	C1-	A1-	35	O										
		_		Ala		-										
	WTW	MGM	CAA	GCA	mı	191										

	(2)		INF	ORMA'					NO:							
			(i)		SEQ	UENC	E CH	ARAC	TERI	STIC	S:					
					(A)		LEN	GTH:	10.	5						
5					(B)				Nucl		Acid					
3					(C)		STR	ANDE	DNES	S:	Sing:	1e				
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			(ii	)	KIN	D: c	DNA	to g	enom	ic R	ΝA					
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10					(A)		SEQ	UENC	E AS	SEMB	LY M	ETHO:	D: (	Over	lap	
10					(B)		FRA	<b>GMEN</b>	T TY	PE:	Int	erna	l Fra	agme	nt	
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			(ii	i)	ORI	GINA	L SO	URCE	: HI	V						
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			(iv	)	IMM	EDIA'	TE S	OURC	E:							
15					(C)		CLO	NE:						_		
			(v)		POS	ITIO	N IN	GEN	OME:	Wit	hin 1	Env (	Gene			
			(vi	)	PRO	PERT	IES (	OF S	equei	NCE:	Ex	pres	ses (	cons	erved	antigenic
					det	ermi	nant									
20			(vi	ii)	SEQ	UENC	E DE	SCRI	PTIO	N:						
20																
	SEQ	ID 1	NO:	EE5	4-1											
25	1				5					10					15	-
		Thr	Ara	Pro		Agn	Agn	Thr	Arg			Ile	Asn	Ile	_	
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35					35											
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40	(2)		INF	ORMA'	TION	FOR	SEQ	ID 1	NO: 1	EEE6	9–1					
			(i)		SEQ	UENC	E CHA	ARAC'	TERI	STIC	s:					
					(A)		LEN	GTH:	10	5						
					(B)		TYP	E: 3	Nucl	eic A	Acid					
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45					(D)		TOP	OLOG	Y: 1	Line	ar					
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5			(ii) (iii) (iv) (v) (vi)	i)	(A) (B) (C) ORIG (E) IMME (C) POSI	IANI; FAIGS	SEQUENT SEQUEN	JENCE MENT OTHET JRCE: IVIDU OURCE VE: GEN(	TYPE TICAL HIV JAL 1 E: ME:	EMBI E: SOLA	Inte	THOI ernal	Fre	onse	nt	antige	nic
			(vii	i)				SCRIE	TION	i:							
15	SEQ	ID N	io:	EEE	59–1												
	1				5					10					15		
20	Cvs	Thr	Arg	Leu	Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile	His	Ile ATA	Gly GGA		
	TGT	AUA	AGG	CIC	AAC	AAC	AAI	AUA	nun	nnn	VGI	VIV	Onz	nin	0021		
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	Pro	G1v	Arg	Ala	Phe	Tyr	Ala	Thr	G1y	Glu	Ile	Ile	G1y	Asp	Ile		
25	CCA	GGG	AGA	GCA	TTT	TAT	GCA	ACA	GGA	GAA	ATA	ATA	GGA	GAT	ATA		
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35			(1)		(A)	OBITO		GTH:	10								
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40			(ii	)	KIN (A)	D (i:			e or			): ETH0:	D:	Over	lap		
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45			(ii	1)	(E)	ė TNA			: HI' UAL		ATE:						
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50					det	ermi	nant										•
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SEQ ID NO: EEE69-2

10 5 - 1 Cys Thr Arg Leu Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly 5 TGT ACA AGA CTC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA 25 20 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile 10 CCA GGG AGA GCA TIT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA 15 Arg Gln Ala Gln Cys AGA CAA GCA CAG TGT INFORMATION FOR SEQ ID NO: EE74-1 (2) 20 SEQUENCE CHARACTERISTICS: LENGTH: 105 (A) TYPE: Nucleic Acid (B) STRANDEDNESS: Single (C) TOPOLOGY: Linear (D) KIND: cDNA to genomic RNA (ii) KIND (if peptide or protein): (ii) SEQUENCE ASSEMBLY METHOD: Overlap (A) FRACMENT TYPE: Internal Fragment (B) HYPOTHETICAL: (C) ORIGINAL SOURCE: HIV 30 (iii) INDIVIDUAL ISOLATE: (E) IMMEDIATE SOURCE: (iv) CLONE: (C) POSITION IN GENOME: Within Env Gene (v) PROPERTIES OF SEQUENCE: Expresses conserved antigenic 35 (vi) determinant SEQUENCE DESCRIPTION: (viii) 40 SEQ ID NO: EE74-1 10 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Asn Ile Gly

TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA AAT ATA GGA

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	Pro	G1 v	Arg	Ala	Phe	Tyr	Thr	Thr	Gly .	Asp	Ile	Ile	G1y	Asp	Ile	
	CCA	CCC	AGA	GCA	TTT	TAT	ACA	ACA	GGA	GAC	ATA	ATA	GGA	GAT	ATA	
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			(vi	) .					eque	NCE:	Ex	pres	ses	CODS	erved	antigenic
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5					(C)		STRA	NDED	ness	: S	ingl	е				
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			(ii)		KIND	: cD	NA t	o ge	nomi	c RN	A .					
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10					(B)		FRAG	MENT	TYP	E:	Inte	rnal	Fra	gmen	t	
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15			(11)		(C)		CLON	E:								
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			(vii	i)	SEQU	JENCE	DES	CRIE	TION	<b>!:</b>						
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	Cys	Thr	Arg	Pro	ASTI	ABU	AAT	YUY	VCV	AAA	ACT	ATA	AAT	ATA	GGA	
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	Pro	GIY	ALR	CCV	THE	TAT	ACA	ACA	GGA	GAC	ATA	ATA	GGA	GAT	ATA	
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	Ara	G1n	Ala	His												
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15 SEQ ID NO: EEE90-1  1	(ii) KIND (if peptide or protein):  (A) SEQUENCE ASSEMBLY METHOD: Overlap  (B) FRACMENT TYPE: Internal Fragment  (C) HYPOTHETICAL:  (iii) ORIGINAL SOURCE: HIV  (E) INDIVIDUAL ISOLATE:  (iv) IMMEDIATE SOURCE:  (C) CLONE:  (v) POSITION IN GENOME: Within Env Gene  (vi) PROPERTIES OF SEQUENCE: Expresses conserved ant determinant  (viii) SEQUENCE DESCRIPTION:	_ :igenic
Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Ala TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GCA  20 25 25 26 27 28 29 29 20 25 25 20 20 25 26 27 28 29 29 20 20 20 20 20 20 20 21 20 20 20 21 21 22 25 26 27 27 28 29 20 20 20 20 21 20 21 21 22 23 24 25 26 27 27 28 29 20 20 20 20 21 21 22 23 24 25 26 27 28 29 20 20 20 21 21 22 25 26 27 27 28 29 20 20 21 21 21 22 23 24 25 26 27 28 29 20 20 21 21 21 22 23 24 25 26 27 28 28 29 20 20 21 21 21 22 23 24 25 26 27 28 28 29 20 20 20 21 21 21 22 23 24 25 26 27 28 28 29 20 20 20 21 21 21 22 23 24 25 26 27 28 28 29 20 20 20 21 21 21 21 21 21 21 21 21 21 21 21 21	NO: EEE90-1	
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20 25 30  Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile CCA GGG AGA GCA TTT TAC GCA ACA GGA GAA ATA ATA GGA GAT ATA  35  Arg Gln Ala His Cys AGA CAA GCA CAT TGT  (2) INFORMATION FOR SEQ ID NO: EE90-2 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 (B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single (D) TOPOLOGY: Linear (ii) KIND: cDNA to genomic RNA (ii) KIND (if peptide or protein): (A) SEQUENCE ASSEMBLY METHOD: Overlap (B) FRAGMENT TYPE: Internal Fragment (C) HYPOTHETICAL: (iii) ORIGINAL SOURCE: HIV (E) INDIVIDUAL ISOLATE: (iv) IMMEDIATE SOURCE: (V) POSITION IN GENOME: Within Env Gene (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigen	<del></del>	
Pro Cly Arg Ala Phe Tyr Ala Thr Cly Clu Ile Ile Cly Asp Ile CCA GGG AGA GCA TTT TAC GCA ACA GGA GAA ATA ATA GGA GAT ATA  35 30 Arg Cln Ala His Cys AGA CAA GCA CAT TGT  (2) INFORMATION FOR SEQ ID NO: EE90-2 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 (B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single (D) TOPOLOGY: Linear (ii) KIND: cDNA to genomic RNA (ii) KIND (if peptide or protein): (A) SEQUENCE ASSEMBLY METHOD: Overlap (B) FRACMENT TYPE: Internal Fragment (C) HYPOTHETICAL: (ii) ORIGINAL SOURCE: HIV (E) INDIVIDUAL ISOLATE: (iv) IMMEDIATE SOURCE: (C) CLONE: (v) POSITION IN GENOME: Within Env Gene (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigen	A AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GCA	
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(viii) SEQUENCE DESCRIPTION:	determinant (viii) SEQUENCE DESCRIPTION:	

SEQ ID NO: EE90-2 5 10 5 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Ala TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GCA 20 25 30 10 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile CCA GGG AGA GCA TTT TAC GCA ACA GGA GAA ATA ATA GGA GAT ATA 35 Arg Gln Ala His Cys AGA CAA GCA CAT TGT (2) INFORMATION FOR SEQ ID NO: EE90-3 20 SEQUENCE CHARACTERISTICS: (i) LENGTH: 105 (A) TYPE: Nucleic Acid (B) STRANDEDNESS: Single (C) TOPOLOGY: Linear (D) (ii) KIND: cDNA to genomic RNA 25 (ii) KIND (if peptide or protein): SEQUENCE ASSEMBLY METHOD: Overlap (A) FRAGMENT TYPE: Internal Fragment (B) (C) HYPOTHETICAL: ORIGINAL SOURCE: HIV 30 (iii) (E) INDIVIDUAL ISOLATE: (iv) IMMEDIATE SOURCE: CLONE: (v) POSITION IN GENOME: Within Env Gene (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic 35 determinant (viii) SEQUENCE DESCRIPTION: SEQ ID NO: EE90-3 40

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Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Ala TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GCA

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10	Pro G CCA G	ly Arg GG AGA	Ala GCA	20 Phe Tyr TTT TAT	Ala Thr GCA ACA	Gly GGA	25 Glu Ile GAA ATA	: Ile ATA	Gly GGA	Asp GAT	30 Ile ATA	
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35	1 Cys	Thr	Arg	Pro	5 Asn	Asn	Asn AAT	Thr ACA	Arg AGA	Lys	G1y GGT	Ile ATA	His CAT	Leu CTA	G1y		
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	1 Cys TGT	Thr ACA	Arg AGA	Pro CCC	5 Asn AAC 20 Phe	Asn AAC Tyr	AAT Ala	ACA	AGA Gly	Lys AAA 25 Glu	GGT Ile	ATA Ile	CAT Gly	CTA	Gly GGA 30 Ile		
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40	1 Cys TGT Pro	Thr ACA Gly GGG	Arg AGA Arg AGA	Pro CCC Ala GCA	5 Asn AAC 20 Phe TTT	Asn AAC Tyr	AAT Ala	ACA	AGA Gly	Lys AAA 25 Glu	GGT Ile	ATA Ile	CAT Gly	CTA	Gly GGA 30 Ile		
40	1 Cys TGT Pro CCA	Thr ACA Gly GGG	Arg AGA Arg AGA	Pro CCC Ala GCA	5 Asn AAC 20 Phe TTT	Asn AAC Tyr TAT	AAT Ala	ACA	AGA Gly	Lys AAA 25 Glu	GGT Ile	ATA Ile	CAT Gly	CTA	Gly GGA 30 Ile		
40	1 Cys TGT Pro CCA	Thr ACA Gly GGG	Arg AGA Arg AGA	Pro CCC Ala GCA	5 Asn AAC 20 Phe TTT	Asn AAC Tyr TAT	AAT Ala	ACA	AGA Gly	Lys AAA 25 Glu	GGT Ile	ATA Ile	CAT Gly	CTA	Gly GGA 30 Ile		
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			(vi)											CORRE	erved	antigenic
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			(vii	ii)				SCRT	PTIO	<b>V</b> :						
20			( •	,	D.L.Q.											
	SEQ	ID P	10:	EE13	31–1											
	•															
25	1				5					10				•	15	
	Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Ser	Lys	Arg	Ile	Ser	Ile	Gly	
	TGT	ACA	AGA	CCC	AAC	AAC	AAT	ACA	AGC	AAA	AGA	ATA	TCT	ATA	GGA	
20																
30					20					25					30	
									Arg							
	CCA	GGG	AGA	GCT	TTT	CGT	GCA	ACA	AGA	ATA	ATA	GGA	GAT	ATA	AGA	
05																
35					35											
	G1n	Ala	His	Cys												
	CAA	GCA	CAT	TGT								,				
:40																
40	(2)		INFO	ORMA'	LION	FOR	SEQ	ID I	NO: 1	EB13	1-2					
			(i)			UENC	E CH	ARAC'	TERI	STIC	S:					
	-				(A)		LEN	GTH:	10	5						
					(B)		TYP	E: 1	Nucle	eic /	Acid					
					(C)		STR	ANDE	DNES:	S: 9	Sing	le				
45					(D)		TOP	OLOG	Y: 3	Line	ar					
			(ii)	)			DNA	to g	enom:	ic RI	NA					
			(ii)						e or			<b>)</b> :				
					(A)				E AS				D:	Over:	lap	
					(B)		-		T TY					agme	-	
50										-				J J		

5			(iii (iv)	)	(C) ORIG (E) IMME (C)	INAL DIAT	SOU INDI E SO CLON	RCE: VIDU URCE	AL I	SOLA						· <del>·········</del>	
			(v) (vi)		PROP dete	ERTI	ES C	)F SE		CE:	in E Exp	nv (	es (	onse	erved	antigeni	c
10			(vii	i)	SEQU	ENCE	DES	CRII	PTION	:							
	SEQ	ID N	10:	EE13	31-2												
15					5					10					15		
	1 Cvs	Thr	Arg	Pro	Agn	Asn	Asn	Thr	Ser	Lys	Arg	Ile	Ser	Ile	Gly CCA		
	TGT	ACA	AGA	CCC	AAC	AAC	AAT	ACA	AGT	AAA	AGĀ	ATA	TCT	ATA	GGA		
20					20					25					30		
	Pro	G1 v	MET	Ala	Phe	Arg	Ala	Thr	Arg	Ile	Ile	G1y	Asp	Ile	Arg		
	CCA	GGG	ATG	GCA	TIT	CGT	GCA	ACA	AGĀ	ATA	ATA	GGA	GAT	ATA	AGA		
25					35												
	Gln	Ala	His	Cys	33					-							•
			CAT														
30	(2)				TION	FOR	SEQ	ID	NO:	EE13	1-3						
			(i)		SEQ (A)		E CH	AKAU GTH:	TERI 10	2 2110	5.						
					(B)		TYP	E:	Nuc1	eic	Acid						
					(C)				DNES		Sing	1e					
35					(D)	<b>D</b>		OLOG	Y: enom	Line							
			(ii (ii		KIN	D: C	pina f pe	ptid	e or	pro	tein	):					
			(11	,	(A)		SEQ	UENC	E AS	SEMB	LY M	ETHO					
					(B)				T TY		Int	erns	1 Fr	agme	mt		
40					(C)				TICA : HI						<del></del>		
			(ii	.1 )	(E)				UAL		ATE:	. <u></u>					
			(iv	·)				OUR									
			-	-	(C)		CTC	NE:				P	0				
45			(v)		POS	ITIC	N II	GE	OME:	Wit	hin P-	EUA.	Gene	COT!	eprve:	d antiger	ic
			iv)	<b>(</b> )		PERI :ermi			LUUL	MACE :	. 52	rhres	9050	COM	JUL 7 61		
		•	iv)	lii)					(PTIC	n:							

SEQ ID NO: EE131-3 10 5 Cys Thr Arg Pro Asn Asn Asn Thr Ser Lys Arg Ile Ser Ile Gly 5 TGT ACA AGA CCC AAC AAC AAT ACA AGC AAA AGA ATA TCT ATA GGA 30 25 Pro Gly Arg Ala Phe Arg Ala Thr Arg Ile Ile Gly Asp Ile Arg CCA GGG AGA GCA TTT CGT GCA ACA AGA ATA ATA GGA GAT ATA AGA 35 15 Gln Ala His Cys CAA GCA CAT TGT INFORMATION FOR SEQ ID NO: EEE149-1 (2) 20 SEQUENCE CHARACTERISTICS: (i) LENGTH: 105 (A) TYPE: Nucleic Acid (B) STRANDEDNESS: Single (C) TOPOLOGY: Linear (D) 25 KIND: cDNA to genomic RNA (ii) KIND (if peptide or protein): (ii) SEQUENCE ASSEMBLY METHOD: Overlap (A) FRACMENT TYPE: Internal Fragment (B) HYPOTHETICAL: (C) 30 ORIGINAL SOURCE: HIV (iii) INDIVIDUAL ISOLATE: IMMEDIATE SOURCE: (iv) CLONE: (C) POSITION IN GENOME: Within Env Gene (v) PROPERTIES OF SEQUENCE: Expresses conserved antigenic 35 (vi) determinant (viii) SEQUENCE DESCRIPTION: SEQ ID NO: EEE149-1

5

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46

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Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Gly Ile Ser Ile Gly TGT ACA AGA CCC AAC AAC AAT ACA AGA AGG GGT ATA AGT ATA GGA

					20					25					30		
	Pro G	ly A	rg A	Ala	Phe	Val	Tyr	Ala	Thr	Lys AAA	Ile	Ile ATA	Gly GGA	Asp GAT	Ile ATA		
	CCA G	GG A	GA (	<i>G</i> CA	111	GII	INI	GUA	AUA	nnn	nin	*****	-				
5					25												
	Arg G	ln A	la l	His	35 Cys												
	AGA C																
10																	
	(2)			RMAT	ION	FOR	SEQ	ID I	NO: E TERIS	E149	)-2 :•						
		(	(i)		SEQU	ENCI	LEN	GTH:	105	<b>;</b>							
15					(B)		TYP:	E: I	Nucle DNESS	ic A	icid	ء ا					
					(D)		TOP	OLOG	Y: I	ine	ır						
			(ii)		KINI	); cl	DNA	to g	enomi	ic RN	IA Tein	١.					
		,	(ii)		(V)	(1.	SEQ	UENC	E ASS	EMBI	LY M	ETHO	D: (	)ver1	lap		
20					(B)				T TYI		Int	erna	l Fra	agmer	ıt		
		(	(iii	)		INA	L SO	URCE	: HIV	7							
		4	(iv)		(E)	ZDTA		IV ID OURC	UAL : E:	(SOL	ATE:						
25		,	(14)			JD 111											
					(C)		CLO							-			
			(v)		POS	TIO	N IN	GEN	OME:	With	nin Ex	Env pres	Gene ses	- conse	erved	antige	nic
		(	(vi)		POS: PROI dete	PERT ermi	N IN IES nant	GEN OF S	EQUE	MCE:	hin Ex	Env pres	Gene ses	conse	erved	antige	nic
30		(	•		POS: PROI dete	PERT ermi	N IN IES nant	GEN OF S	OME: EQUE PTIO	MCE:	nin Ex	Env pres	Gene ses	conse	erved	antige	nic
30	SEQ 1	(	(vi) (vii	i)	POS: PROI deto SEQI	PERT ermi	N IN IES nant	GEN OF S	EQUE	MCE:	in Ex	Env pres	Gene ses	conse	erved	antige	nic
30	SEQ 1	(	(vi) (vii	i)	POS: PROI deto SEQI	PERT ermi	N IN IES nant	GEN OF S	EQUE	NCE:	Ex	Env pres	Gene ses	- conse		antige	enic
30 35	1	ID N	(vi) (vii 0:	i) EE14	POS: PROI dete SEQU	PERT ermi JENC	N IN IES nant E DE	GEN OF S	EQUEI PTIOI	NCE: N: 10	Ex	pres	ses	conse	15	antige	nic
	-	ID No	(vi) (vii 0: Arg	i) EE14 Pro	POS: PROI dete SEQI 49-2	PERT ermi JENC	N IN IES nant E DE	GEN OF S SCRI	EQUEI PTIOI	VCE: N: 10 Arg	Ex	pres Ile	ses	conse Ile	15 Gly	antige	enic
	1 Cvs T	ID No	(vi) (vii 0: Arg	i) EE14 Pro	POS: PROI dete SEQI 49-2	PERT ermi JENC	N IN IES nant E DE	GEN OF S SCRI	EQUEI PTIOI	VCE: N: 10 Arg	Ex	pres Ile	ses	conse Ile	15 Gly	antige	enic
<b>35</b>	1 Cys T	ID No	(vi) (vii O: Arg AGA	i) EE14 Pro	POS: PROI dete SEQI 49-2 5 Asn AAC	PERT ermi UENC Asn AAC	N IN IES nant E DE	GEN OF S SCRI	EQUEI PTIOI Arg	NCE: N: 10 Arg AGG	G1y GGT	Ile ATA	ses Ser	Ile ATA	15 G1y GGA	antige	mic
	1 Cys T TGT A	ID No	(vi) (vii 0: Arg AGA	i) EE14 Pro CCC	POS: PROI detc SEQI 49-2 5 Asn AAC	PERT Exmi JENC Asn AAC	N IN IES nant E DE	GEN OF S SCRI	PTIO	NCE: N: 10 Arg AGG 25 Lys	Gly GGT	Ile ATA	ses Ser AGT	Ile ATA	15 Gly GGA 30 Ile	antige	mic
<b>35</b>	1 Cys T	ID No	(vi) (vii 0: Arg AGA	i) EE14 Pro CCC	POS: PROI detc SEQI 49-2 5 Asn AAC	PERT Exmi JENC Asn AAC	N IN IES nant E DE	GEN OF S SCRI	PTIO	NCE: N: 10 Arg AGG 25 Lys	Gly GGT	Ile ATA	ses Ser AGT	Ile ATA	15 Gly GGA 30 Ile	antige	mic
35 , 40	1 Cys T TGT A	ID No	(vi) (vii 0: Arg AGA	i) EE14 Pro CCC	POS: PROI detc SEQI 49-2 5 Asn AAC	Asn AAC	N IN IES nant E DE	GEN OF S SCRI	PTIO	NCE: N: 10 Arg AGG 25 Lys	Gly GGT	Ile ATA	ses Ser AGT	Ile ATA	15 Gly GGA 30 Ile	antige	mic
<b>35</b>	1 Cys 7 TGT A	Thr AACA AGGGGG .	(vi) (vii) 0: Arg AGA Arg AAGA	i) EE14 Pro CCC Ala GCA	POS: PROI detc SEQI 49-2 5 Asn AAC 20 Phe TTT	Asn AAC Val	N IN IES nant E DE	GEN OF S SCRI	PTIO	NCE: N: 10 Arg AGG 25 Lys	Gly GGT	Ile ATA	ses Ser AGT	Ile ATA	15 Gly GGA 30 Ile	antige	mic
35 , 40	1 Cys 7 TGT A	Thr AACA AGGGGG .	(vi) (vii) 0: Arg AGA Arg AAGA	i) EE14 Pro CCC Ala GCA	POS: PROI detc SEQI 49-2 5 Asn AAC 20 Phe TTT	Asn AAC Val	N IN IES nant E DE	GEN OF S SCRI	PTIO	NCE: N: 10 Arg AGG 25 Lys	Gly GGT	Ile ATA	ses Ser AGT	Ile ATA	15 Gly GGA 30 Ile	antige	mic

	(2)		TION FOR SEQ ID NO: EE149-3	
		(i)	SEQUENCE CHARACTERISTICS:	
			(A) LENGTH: 105	
			(B) TYPE: Nucleic Acid	
5			(C) STRANDEDNESS: Single	
			(D) TOPOLOGY: Linear	
		(ii)	KIND: cDNA to genomic RNA	
		(ii)	KIND (if peptide or protein):	
			(A) SEQUENCE ASSEMBLY METHOD: Overlap	
10			(B) FRACMENT TYPE: Internal Fragment	
			(C) HYPOTHETICAL:	
		(iii)	ORIGINAL SOURCE: HIV	
			(E) INDIVIDUAL ISOLATE:	
		(iv)	IMMEDIATE SOURCE:	
15			(C) CLONE:	
		(v)	POSITION IN GENOME: Within Env Gene	
		(vi)	PROPERTIES OF SEQUENCE: Expresses conserved antigenic	C
			determinant	
		(viii)	SEQUENCE DESCRIPTION:	
20			•	
	SEQ ID	NO: BE1	49–3	
25	1		5 10 15	
			Asn Asn Asn Thr Arg Arg Gly Ile Ser Ile Gly	
	TGT AC	A AGA CCC	: AAC AAC AAT ACA AGA AGG GGT ATA AGT ATA GGA	
30			20 25 30	
			Phe Val Tyr Ala Thr Lys Ile Ile Gly Asp Ile	
	CCA GG	G AGA GCA	A TIT GIT TAT GCA ACA AAA ATA ATA GGA GAT ATA	
35			35	
		n Ala His		
	AGA CA	A GCA CAT	TGT	
40	(2)		TION FOR SEQ ID NO: EEE159-1	
		(i)	SEQUENCE CHARACTERISTICS:	
•			(A) LENGTH: 105	
			(B) TYPE: Nucleic Acid	
			(C) STRANDEDNESS: Single	
45			(D) TOPOLOGY: Linear	
		(ii)	KIND: cDNA to genomic RNA	
		(ii)	KIND (if peptide or protein):	
			(A) SEQUENCE ASSEMBLY METHOD: Overlap	
			(B) FRAGMENT TYPE: Internal Fragment	
50				

			(iii	)	(C)	INAL			CICAL HIV						<del></del>		
					(E)		IND	VIDU	JAL I		TE:					<del></del>	
5			(iv)	)	(C)	TAIG	CLO	IE:						_			
			(v)			TION											
			(vi)	)	dete	ermin	ant				EXI	press	ses c	conse	ervea	antigenio	•
10			(vi	i <b>i)</b>	SEQU	JENCE	DES	SCRII	PTION	<b>:</b>							
	SEQ	ID I	:ON	EEE	L59-1	l											
15	1				5					10					15		
	Cvs	Thr	Arg	Pro	Ser	Asn	Asn	Thr	Arg	Lys	Ser	Ile	His	Ile	G1 <b>y</b>		
	TGT	ACA	AGĂ	CCC	AGC	AAC	AAT	ACA	AGA	AAA	AGT	ATA	CAT	ATA	GGA		
20					20					25					30		
	Pro	Glv	Arg	Ala	Phe	Tyr	Ala	Thr	G1y	Glu	Ile	Ile	G1y	Asp	Ile		
	CCA	GGG	AGA	GCA	TTT	TAT	GCA	ACA	GGA	GAA	ATA	ATA	GGA	GAT	ATA		
25					35												
			Ala														
	AGA	CAA	GCA	CAT	TGT												
30	(2)				TION	FOR	SEQ	ID I	NO:	EEE1	59-2						
		•	(i)		SEQ!	UENC		ARAC GTH:			s:						
					(B)				Nucl		Acid						
35					(C)				DNES			1e					
30					(D)				Y:								
			(ii (ii			D: cl D (i:						):					
			(11	,	(A)		SEQ	UENC	E AS	SEMB	LY M	ETHO					
40					(B)				T TY		Int	erna	1 Fr	agme	nt		
40			/11	2 )	(C)	GINA			TICA								
			ii)	1)	(E)				UAL		ATE:						
			(iv	)	IMM	EDIA	TE S	OURC									
45					(C)		CLO			1.1.2 4	<u> </u>	E	Con				
			(v) (vi		PDS	ITIO	IRC N IN	OF S	ROUE:	WIT •NCE	nin Ev	Dres Dres	ees Gene	CORS	erved	antigeni	.c
			(V1	,		ermi			-40B			·F- ~0					_
			(vi	ii)		UENC			PTIO	N:							

SEQ ID NO: EEE159-2

					5					10					15		
5	1		<b>A</b>	D	) Ann	A 0.00	Acn	The	Arg		Ser	I1e	Pro	I1e	G1v		
3	Cys	Thr	Arg	rro	ABU	WRIT	AAT	YUY	VCC		AGT	ATA	CCT	ATA	GGA		
	TGT	ACA	AGA	CCC	AAC	AAC	w	nun	noo								
					20					25					30		
10	D	Clar	Ara	ΔΙα	Phe	Tvr	Ala	Thr	G1y		Ile	Ile	G1y	Asp	I1e		
10	LLO	CCC	VCV UTR	CCA	Julia LTIC	TAT	GCA	ACA	GGA	GAC	ATA	ATA	GGA	GAT	ATA		
	CUA	999	non	0022													
					35												
15	Ara	Cln	Ala	His													
				CAT													
	tion	OLM.	00.	<b></b>													
	(2)		INF	)RMAT	CION	FOR	SEQ	ID :	NO:	EE159	9~3						
20	<b>\</b> >		(i)		SEQ	JENC	E CH	ARAC	TERI	STIC	S:						
			-		(A)			GTH:		-							
					(B)				Nucl								
					(C)				DNES			le					
					(D)				Y:								
25			(ii		KIN	D: c	DNA	to g	enom	ic R	NA .						
			(ii	•	KIN	D (†	f ne	ntid	e or	pro	tein	):					
			(	,			- P-	r	_ :_				_	A	4		
			(	,	(A)		SEQ	UENC	E AS	SEMB:	LY M	CHT	D:	0ver	lap		
			(11	,	(A) (B)		SEQ FRA	UENC GMEN	E AS T TY	SEMB PE:	LY M	CHT	D: 1 Fr	Over agme	lap nt		
					(A) (B) (C)		SEQ FRA HYP	UENC GMEN OTHE	E AS T TY TICA	SEMB: PE: L:	LY M	CHT	D: 1 Fr	Over agme	lap nt		
30			(ii		(A) (B) (C) ORI	GINA	SEQ FRA HYP L SO	UENC GMEN OTHE URCE	E AS T TY TICA : HI	SEMB PE: L: V	Into	erna	D: 1 Fr	Over agme	lap nt		
30			(ii	i)	(A) (B) (C) ORI (E)	GINA	SEQ FRA HYP L SO IND	UENC GMEN OTHE URCE IVID	E AS T TY TICA : HI UAL	SEMB PE: L: V	Into	erna	D: 1 Fr	Over agme	lap nt		
30				i)	(A) (B) (C) ORIC (E) IMM	GINA EDIA	SEQ FRA HYP L SO IND TE S	UENC GMEN OTHE URCE IVID	E AS T TY TICA : HI UAL	SEMB PE: L: V	Into	erna	D: 1 Fr	Over agme	lap nt		
30			(ii	i)	(A) (B) (C) ORI (E) IMM (C)	GINA EDIA	SEQ FRA HYP L SO IND TE S CLO	UENC GMEN OTHE URCE IVID OURC	E AS T TY TICA : HI UAL E:	SEMB PE: L: V ISOL	LY Mi Into	erna	1 Fr	agme	lap nt		
			(ii (iv (v)	i)	(A) (B) (C) ORI (E) IMM (C) POS	GINA EDIA ITIO	SEQ FRA HYP L SO IND TE S CLO N IN	UENC GMEN OTHE URCE IVIE OURC NE:	E AS T TY TICA : HI UAL E:	SEMB: PE: L: V ISOL	LY Mi Into	Env	Gene	agme	nt 		_
30 35			(ii	i)	(A) (B) (C) ORIGORY (E) IMM (C) POS PRO	GINA EDIA ITIO PERT	SEQ FRA HYP L SO IND TE S CLO N IN	UENC GMEN OTHE URCE IVIE OURC INE: GEN OF S	E AS T TY TICA : HI UAL E:	SEMB: PE: L: V ISOL	LY Mi Into	Env	Gene	agme	nt 	antigenio	•
			(ii (iv (v) (vi	i) ) )	(A) (B) (C) ORI (E) IMM (C) POS PRO det	GINA EDIA ITIO PERT ermi	SEQ FRA HYP L SO IND TE S CLO N IN IES nant	UENC GMEN OTHE URCE OURC OURC NE: GEN	E AS T TY TICA : HI OUAL E: OME: EQUE	SEMB PE: L: V ISOL Wit	LY Mi Into	Env	Gene	agme	nt 	antigenio	•
			(ii (iv (v) (vi	i)	(A) (B) (C) ORI (E) IMM (C) POS PRO det	GINA EDIA ITIO PERT ermi	SEQ FRA HYP L SO IND TE S CLO N IN IES nant	UENC GMEN OTHE URCE OURC OURC NE: GEN	E AS T TY TICA : HI UAL E:	SEMB PE: L: V ISOL Wit	LY Mi Into	Env	Gene	agme	nt 	antigenio	3
			(ii (iv (v) (vi	i) ) )	(A) (B) (C) ORI (E) IMM (C) POS PRO det	GINA EDIA ITIO PERT ermi	SEQ FRA HYP L SO IND TE S CLO N IN IES nant	UENC GMEN OTHE URCE OURC OURC NE: GEN	E AS T TY TICA : HI OUAL E: OME: EQUE	SEMB PE: L: V ISOL Wit	LY Mi Into	Env	Gene	agme	nt 	antigenio	2
35	กสอ	TD.	(ii (iv (v) (vi (vi	i) ) ii)	(A) (B) (C) ORI (E) IMM (C) POS PRO det SEQ	GINA EDIA ITIO PERT ermi UENC	SEQ FRA HYP L SO IND TE S CLO N IN IES nant	UENC GMEN OTHE URCE OURC OURC NE: GEN	E AS T TY TICA : HI OUAL E: OME: EQUE	SEMB PE: L: V ISOL Wit	LY Mi Into	Env	Gene	agme	nt 	antigenio	>
	SEQ	ID	(ii (iv (v) (vi (vi	i) ) )	(A) (B) (C) ORI (E) IMM (C) POS PRO det SEQ	GINA EDIA ITIO PERT ermi UENC	SEQ FRA HYP L SO IND TE S CLO N IN IES nant	UENC GMEN OTHE URCE OURC OURC NE: GEN	E AS T TY TICA : HI OUAL E: OME: EQUE	SEMB PE: L: V ISOL Wit	LY Mi Into	Env	Gene	agme	nt 	antigenio	2
35	SEQ	, ID	(ii (iv (v) (vi (vi	i) ) ii)	(A) (B) (C) ORI (E) IMM (C) POS PRO det SEQ	GINA EDIA ITIO PERT ermi UENC	SEQ FRA HYP L SO IND TE S CLO N IN IES nant	UENC GMEN OTHE URCE OURC OURC NE: GEN	E AS T TY TICA : HI OUAL E: OME: EQUE	SEMB PE: L: V ISOL Wit	LY Mi Into	Env	Gene	agme	nt 	antigenio	2
35	1		(ii (iv (v) (vi (vi	i) ) ii) EE1	(A) (B) (C) ORI (E) IMM (C) POS PRO det SEQ	GINA EDIA ITIO PERT ermi UENC	SEQ FRA HYP L SO IND TE S CLO N IN IES nant E DE	UENC GMEN OTHE URCE UVID OURCE NE: GEN OF S	E AS T TY TICA : HI DUAL :E: COME: EQUE	SEMB PE: L: V ISOL Wit NCE:	ATE:	Env pres	Geneses	cons	served	antigenio	2
35	1 TGT	' ACA	(ii (iv (v) (vi (vi	i) ) ii) EEL	(A) (B) (C) ORI (E) IMM (C) POS PRO det SEQ	GINA EDIA ITIO PERT ermi UENC	SEQ FRA HYP L SO IND TE S CLO N IN IES nant E DE	UENC GMEN OTHE URCE UVID OURCE NE: GEN OF S	E AS T TY TICA : HI UAL :E: COME: EQUE	SEMB PE: L: V ISOL Wit NCE:	ATE:	Env Pres	Genesses	cons	erved	antigenio	3
35 40	1 TGT	' ACA	(ii (iv (v) (vi (vi	i) ) ii) EEL	(A) (B) (C) ORI (E) IMM (C) POS PRO det SEQ	GINA EDIA ITIO PERT ermi UENC	SEQ FRA HYP L SO IND TE S CLO N IN IES nant E DE	UENC GMEN OTHE URCE UVID OURCE NE: GEN OF S	E AS T TY TICA : HI UAL :E: COME: EQUE	SEMB PE: L: V ISOL Wit NCE:	ATE:	Env Pres	Genesses	cons	erved	antigenio	2
35	1 TGT	' ACA	(ii (iv (v) (vi (vi	i) ) ii) EEL	(A) (B) (C) ORI (E) IMM (C) POS PRO det SEQ	GINA EDIA ITIO PERT ermi UENC	SEQ FRA HYP L SO IND TE S CLO N IN IES nant E DE	UENC GMEN OTHE URCE UVID OURCE NE: GEN OF S	E AS T TY TICA : HI UAL :E: COME: EQUE	SEMB PE: L: V ISOL Wit NCE:	ATE:	Env Pres	Genesses	cons	served	l antigenio	2
35 40	1 TGT	' ACA	(ii (iv (v) (vi (vi	i) ) ii) EEL	(A) (B) (C) ORI (E) IMM (C) POS PRO det SEQ	GINA EDIA ITIO PERT ermi UENC	SEQ FRA HYP L SO IND TE S CLO N IN IES nant E DE	UENC GMEN OTHE URCE UVID OURCE NE: GEN OF S	E AS T TY TICA : HI UAL :E: COME: EQUE	SEMB PE: L: V ISOL Wit NCE:	ATE:	Env Pres	Genesses	cons	15 A GGA	antigenio	:
35 40	1 TGT Cys	ACA	(ii (iv (v) (vi (vi NO:	i) ) ii) EE1 CCC Pro	(A) (B) (C) ORI (E) IMM (C) POS PRO det SEQ 59-3	GINA EDIA ITIO PERT ermi UENC	SEQ FRA HYP L SO IND TE S CLO N IN IES nant E DE	UENC GMEN OTHE URCE OURC ONE: GEN OF S SCRI	E AS T TY TICA : HI OUAL :E: COME: EQUE TPTIO	SEMB PE: L: V ISOL Wit NCE: N:	ATE: hin Ex	Env Env ATA	Geneses	cons	15 A GGA e Gly	antigenio	3
35 40	1 TGT Cys	' ACA	(ii (iv (v) (vi (vi NO:	i) ) ii) EE1 CCC Pro	(A) (B) (C) ORI (E) IMM (C) POS PRO det SEQ 59-3	GINA EDIA ITIO PERT ermi UENC Asn	SEQUENT SEQUEN	UENC GMEN OTHE URCE OURC ONE: GEN OF S SCRI	E AS T TY TICA : HI OUAL :E: COME: EQUE TPTIO	SEMB PE: L: V ISOL Wit NCE: N:	ATE: hin Ex	Env Env ATA	Geneses	CODE	15 A GGA e Gly	antigenio	:
35 40	1 TGT Cys	' ACA	(ii (iv (v) (vi (vi NO:	i) ) ii) EE1 CCC Pro	(A) (B) (C) ORI (E) IMM (C) POS PRO det SEQ 59-3	GINA EDIA ITIO PERT ermi UENC Asn	SEQUENT SEQUEN	UENC GMEN OTHE URCE OURC ONE: GEN OF S SCRI	E AS T TY TICA : HI OUAL :E: COME: EQUE TPTIO	SEMB PE: L: V ISOL Wit NCE: N:	ATE: hin Ex	Env Env ATA	Geneses	CODE	15 A GGA e Gly	antigenio	3

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	AGA	CAA	GCA	CAT													
	Arg	Gln	Ala	His	Cys												
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5																	
	(2)			ORMA'						EE164							
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					(D)	۰۱											
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			(ii	,	(A)	) (1)				PLO: SEMBI			). (	wer	lan ·		
15					(B)					PE:							
					(c)				rica)					-6			
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			,	-,	(E)					ISOL	ATE:						_
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20			•		(C)		CLO	VE:						_			
			(v)							Witl							
			(vi	)	PRO	PERT	CES (	OF S	EQUE	NCE:	Exp	pres	ses (	cons	erved	ant	igenic
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			(vi	ii)	SEQ	JENC	E DES	SCRI	PTIO	N:							
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	220	-n :		DD1/													
	SEQ	ו עו	NU:	EE10	)4-L												
30	1				5				•	10					15		
	Cvs	Thr	Arg	Pro	Ser	Asn	Asn	Thr	Ser	Lys	G1y	Ile	His	Ile	G1y		
	TGT	ACA	AGA	CCC	AGC	AAC	AAT	ACA	AGC	AAA	GGT	ATA	CAT	ATA	GGA		
35					20					25					30		
	Pro	G1y	Arg	Ala	Phe	Tyr	Thr	Thr	G1y	Asn	Ile	Ile	Gly	Asn	Ile		
	CCA	GGG	AGA	GCA	TTT	TAT	ACA	ACA	GGA	AAT	ATA	ATA	GGA	TAA	ATA		
40					25												
70	<b>A</b>	01-	41.	111.	35												
				His CAT													
	AGA	UMA	GUA	CAI	161												
45	(2)		INF	ORMA'	rion	FOR	SEQ	ID I	NO:	EE16	4-2						
			(i)							STIC							
					(A)			GTH:	10								
					(B)		TYP	<b>E:</b> 1	Nuc1	eic	Acid						
50																	

			(C) STRANDEDNESS: Single (D) TOPOLOGY: Linear
5		(ii) (ii)	KIND: cDNA to genomic RNA KIND (if peptide or protein): (A) SEQUENCE ASSEMBLY METHOD: Overlap (B) FRACMENT TYPE: Internal Fragment (C) HYPOTHETICAL:
10		(iii) (iv)	(C) HYPOTHETICAL: ORIGINAL SOURCE: HIV (E) INDIVIDUAL ISOLATE: IMMEDIATE SOURCE: (C) CLONE:
		(v) (vi)	POSITION IN GENOME: Within Env Gene PROPERTIES OF SEQUENCE: Expresses conserved antigenic
15		(viii)	determinant SEQUENCE DESCRIPTION:
20	SEQ ID	NO: EE1	64–2
	ì		5 10 15
	Cys Thr TGT ACA	Arg Pro AGA CCC	Asn Asn Asn Thr Ser Arg Gly Ile His Ile Gly AAC AAC AAT ACA AGC AGA GGT ATA CAT ATA GGA
25			
	Pro Gly	Arg Ala	20 25 30 Phe Tyr Ala Thr Gly Asn Ile Ile Gly Asp Ile
30	CCA GGG	AGA GCA	TTT TAT GCA ACA GGA AAT ATA ATA GGA GAT ATA
		.1 71	35
		Ala His GCA CAT	
35	4-3		
,	(2)	INFORMA	TION FOR SEQ ID NO: EEE164-3 SEQUENCE CHARACTERISTICS:
40			(A) LENGTH: 105 (B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single (D) TOPOLOGY: Linear
<b>4</b> 5		(ii) (ii)	KIND: cDNA to genomic RNA KIND (if peptide or protein): (A) SEQUENCE ASSEMBLY METHOD: Overlap (B) FRAGMENT TYPE: Internal Fragment (C) HYPOTHETICAL:

		(iii)	ORIGINAL SOURCE: HIV (E) INDIVIDUAL ISOLATE:
		(iv)	IMMEDIATE SOURCE: (C) CLONE:
5		(v) (vi)	POSITION IN GENOME: Within Env Gene PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
		(viii)	SEQUENCE DESCRIPTION:
10			
	SEQ ID	NO: EEE	164–3
	1		5 10 15
15	Cys Thr	Arg Pro	Ser Asn Asn Thr Arg Lys Gly Ile His Ile Gly
	TGT ACA	AGA CCC	AGC AAC AAT ACA AGA AAA GGT ATA CAT ATA GGA
			20 25 30
20	Pro Gly	Arg Ala	Phe Tyr Thr Gly Gln Ile Ile Gly Asp Ile
	CCA GGG	AGA GCA	TIT TAT ACA ACA GGA CAA ATA ATA GGA GAT ATA
25			35
25		Ala His	
	AGA CAA	GCA CAT	TGT
30	(2)	INFORMA'	TION FOR SEQ ID NO: EE179-1 SEQUENCE CHARACTERISTICS:
•		(1)	(A) LENGTH: 105
			(B) TYPE: Nucleic Acid
-			(C) STRANDEDNESS: Single
35			(D) TOPOLOGY: Linear
55		(ii) (ii)	KIND: cDNA to genomic RNA KIND (if peptide or protein):
		(11)	(A) SEQUENCE ASSEMBLY METHOD: Overlap
			(B) FRACMENT TYPE: Internal Fragment
			(C) HYPOTHETICAL:
40		(iii)	ORIGINAL SOURCE: HIV
		(:)	(E) INDIVIDUAL ISOLATE:
		(iv)	(C) CLONE:
		(v)	POSITION IN GENOME: Within Env Gene
45		(vi)	PROPERTIES OF SEQUENCE: Expresses conserved antigenic
			determinant
		(viii)	SEQUENCE DESCRIPTION:

SEQ ID NO: EE179-1

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10 5 5 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA 25 20 10 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asn Ile CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA AAT ATA 35 15 Arg Gln Ala His Cys AGA CAA GCA CAC TGT INFORMATION FOR SEQ ID NO: EE179-2 (2) 20 SEQUENCE CHARACTERISTICS: (i) LENGTH: 105 (A) TYPE: Nucleic Acid (B) STRANDEDNESS: Single (C) TOPOLOGY: Linear (D) KIND: cDNA to genomic RNA (ii) KIND (if peptide or protein): (ii) SEQUENCE ASSEMBLY METHOD: Overlap (A) FRAGMENT TYPE: Internal Fragment (B) HYPOTHETICAL: (C) 30 ORIGINAL SOURCE: HIV (iii) INDIVIDUAL ISOLATE: (E) IMMEDIATE SOURCE: (iv) CLONE: (C) POSITION IN GENOME: Within Env Gene (v) 35 PROPERTIES OF SEQUENCE: Expresses conserved antigenic (vi) determinant SEQUENCE DESCRIPTION: (viii) 40 SEQ ID NO: EE179-2 Cys Thr Arg Pro Ser Asn Asn Thr Arg Lys Ser Ile His Ile Gly 45 TGT ACA AGA CCC AGC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

					20					25					30	
	Pro	G1 v	Arg	Ala	Phe	Tyr	Thr	Thr	G1y	Glu	Ile	Ile	Glu	Asn	Ile	
	CCA	GGG	AGA	GCA	TTT	TAT	ACA	ACA	GGA	GAA .	ATA	ATA	GAA	AAT	ATA	
_																
5																
					35											
	Arg	Gln	Ala	His	Cys					•						
	AGA	CAA	GCA	CAC	TGT											•
10																
	(0)		TMEO	TAMO	TON	EUB	SRO	ID N	n: F	R179	-3					
	(2)		(i)	KLINI	SEOU	ENCI	E CHA	ARACT	ERIS	TICS	:					
			(1)		(A)	22.0.		GTH:		5						
					(B)			E: N		ic A	cid					
15					(c)			ANDEI				le				
					(D)			OLOGI								
			(ii)	)	KINI	): cl	DNA	to ge	nomi	c RN	ΙA	_				
			(ii)		KINI	) (i:	f pe	ptide	or	prot	ein	): 			•	
00					(A)		SEQ	UENCI	SASS	SEMBI	M Y.	ETHO	0: (	Over	Iap	
20					(B)		FRA	GMEN?	TYI	?E:	Int	erna.	l Fr	agme	nt	
					(C)			OTHE:								
			(iii	i)		JINA	LSU	URCE:	TAT .	V Tent A	\TE-					
			(1		(E)	2DTA		OURC		LOUIR	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,					
25			(iv)	,	(C)	M'IU	CLO		•					_		
			(v)		POS	מדדמ	N IN	GEN	ME:	With	nin	Env	Gene	_		-
			(vi		PRO	PERT	IES	OF S	EQUE	NCE:	Ex	pres	ses	cons	erved	antigenic
				ì			nant		-							
			(vi:	ii)	SEQ	UENC	E DE	SCRI	PTIO	N:						
30													•			
	SEQ	ID	NO:	EE1	79–3											•
35					5					10					15	
	1	Trib.		Den	Acn	Δот	Aen	Thr	Are			· Ile	His	: I1e	Gly	
	TOT	TITE	VGV WrR	CCC	AAC	AAC	: AAT	ACA	AGA	AAA	AGI	' ATA	CAT	ATA	GGA	
	161	AUF	, non	000	1110											
40					20					25					30	
	Pro	G1 <sub>3</sub>	Arg	Ala	Phe	Ty	The	Thr	Gly	Glu	. I1e	: Ile	: Gly	7 Ası	ı Ile	
	CCA	GGC	AGA	GCA	TTT	'TAT	CACA	A ACA	GGA	GAA	ATA	ATA	GGA	AA:	ATA 1	•
45																
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			Ala													
	AGA	CA	A GCA	CAC	IGI	-										
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	(2)		INFO	RMAT	ION I	FOR	SEQ	ID N	0: E	EE18	1-1						
	1		(i)		SEQU						:						
					(A)		LENG		105								
_					(B)				uc1e								
5					(C)				NESS		ingl	е					
					(D)		TOPO	LOGY	: L	inea							
			(ii)		KIND	: cI	NA t	o ge	nomi	c RN	Α						
			(ii)		KIND	(if	per	tide	or	prot	ein)	:		1			
					(A)				ASS		Y ME	THOD	: U	veri	.ap		
10					(B)				TYP		Inte	rnal	Fra	gmen	I C		
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			(iii	.)	ORIG	INAI											
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15					(C)		CLO	Æ:			<del></del>			-			
			(v)		POSI	TION	IN	GEN	ME:	With	iin k	inv 6	ene			. onticonic	
			(vi)	)				)F SI	<b>zónr</b> i	ICE:	EXI	ress	es c	:UIISt	:Lvec	i antigenio	
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			(vii	li)	SEQU	ENC	E DES	SCR11	PTIO	ł:							
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	SEQ	ID 1	10:	EEE!	L81-1												
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	1	The	Ara	Pro	Asn	Agn	Asn	Thr	Arg	Lvs	Ser	Ile	His	Ile	G1y	•	
	TUT	ACA	ACA	CCC	AAC	AAT	AAT	ACA	AGA	AAA	AGT	ATA	CAT	ATA	GGA		
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	Pro	Gly	Arg	Ala	Phe TTT	lyr	Inr	TOT	GLA	GIU	ATA	ATA	CCA	AAT	ATA		
	CCA	GGG	AGA	GCA	TIT	TAI	AUA	ACG	GGA	GAA	AIA	nin	-			•	
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35					35												
	A	C1n	Ala	Hie													
			GCA														
	AGA	Chin	6021	0.11													
40	(2)		INF	ORMA	TION	FOR	SEQ	ID	NO:	EE18	1-2						
	• •		(i)		SEQ	UENC	E CH	ARAC	TERI	STIC	s:						
					(A)		LEN	IGTH:		· .							
					(B)		TYE		Nuc1		_	_					
					(C)				DNES		Sing	le:					
45					(D)				SY:								
			(ii	.)	KIN	D: c	:DNA	to g	genon	ic R	NA						

5			(ii (ii: (iv) (v)	i)	(A) (B) (C) ORIC (E) IMMI (C)	GINA! EDIA:	SEQUENT SOLUTION OF SOLUTION O	OTHE: URCE IVID OURC	E AS: F TY: FICAL : HIV UAL : E:	SEMB PE: L: V ISOL	Into	erna	l Fr	Over agmen	•		- · ·
10			(vi		PRO!	PERT: ermi:	IES ( nant		EQUEI	NCE:					erve	d ant	igenic
15	SEQ	ID 1	<b>NO:</b>	EE18	31–2												
	1				5					10					15		
		Thr	Arg	Pro		Asn	Asn	Thr	Arg		Ser	Ile	His	Ile		•	
20	TGT	ACA	AGA	CCC	AAC	AAC	AAT	ACA	AGA	AAA	AGT	ATA	CAT	ATA	GGA		
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	Pro	G1 v	Arg	Ala		Tvr	Thr	Thr	Glv		Ile	Ile	G1y	Asn			
25	CCA	GGG	AGA	GCA	TTT	TAT	ACA	ACG	GGA	GAA	ATA	ATA	GGA	AAT	ATA		
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35			(2)		(A)			GTH:	10		•						
					(B)		TYP	E: 1	Nucl	eic /	Acid						
,					(C)			ANDE			Sing	le .					
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40			(ii					ptid				):					
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45			(ii	i)				URCE			۸ TC .			•	•		
			(iv	)	(E)			IVID OURC		TOOF	utr:						
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			(v)		POS	ITIO	N IN	GEN									
50			(vi	)					EQUE	NCE:	Ex	pres	ses			d an	tigenic
50			(vi	ii)		ermi UENC		SCRI	PTIO	N:				1 ½		•	

SEQ ID NO: EE181-3

1 5 10 15
Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly
TGT ACA AGA CCC AAC AAT AAT ACA AGA AAA AGT ATA CAT ATA GGA

Pro Gly Arg Ala Phe Tyr Thr Thr Gly Gly Ile Ile Gly Asp Ile CCA GGG AGA GCA TIT TAT ACA ACG GGA GGA ATA ATA GGA GAT ATA

Arg Gln Ala His Cys AGA CAA GCA CAT TGT

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- INFORMATION FOR SEQ ID NO: EE211-1 (2) SEQUENCE CHARACTERISTICS: (i) LENGTH: 105 (A) TYPE: Nucleic Acid (B) STRANDEDNESS: Single (C) TOPOLOGY: Linear (D) KIND: cDNA to genomic RNA (ii) KIND (if peptide or protein): (ii) SEQUENCE ASSEMBLY METHOD: Overlap (A) FRACMENT TYPE: Internal Fragment (B) HYPOTHETICAL: (C) ORIGINAL SOURCE: HIV (iii) INDIVIDUAL ISOLATE: IMMEDIATE SOURCE: (iv) CLONE: (C) POSITION IN GENOME: Within Env Gene (v) PROPERTIES OF SEQUENCE: Expresses conserved antigenic (vi)
- SEQ ID NO: EE211-1

1 5 10 15

Cys Thr Arg Pro Asn Asp Asn Thr Arg Arg Ser Ile Asn Ile Gly
TGT ACA AGA CCC AAC GAC AAT ACA AGA AGA AGT ATA AAT ATA GGA

determinant (viii) SEQUENCE DESCRIPTION:

					20					25					30			
	Pro	G1v	Arg	Ala	Phe	Tyr	Ala	Thr	Gly	Glu	Ile	Ile	G1y	Asn	Ile.			
	CCA	GGG	AGA	GCC	TTT	TAT	GCA	ACA	GGA	GAA .	ATA	ATA	GGA	AAT	ATA			
	00																	
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					35													
	Aro	Gin	A1a	His														
				CAT														
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	(2)		INF	ORMA'	CION	FOR	SEQ	ID 1	10: E	EE21	1-2							
	\-/		(i)		SEO	JENC!	E CHA	ARAC'	TERIS	TICS	:							
			(-,		(A)			GTH:										
					(B)			E: 1			cid							
15					(c)			ANDEI			ing	le						
					(D)			OLOG		inea	r							
			(ii	)				to ge		c RN	IA.							
			(ii		KTN	) (i	f pe	ptide	or	prot	ein	<b>)</b> :						
			(	,	(A)		SEO	UENC	Z ASS	EMBI	Y M	THO	): (	)ver	lap			
20					(B)		FRA	CMEN.	TYI	E:	Inte	erna	l Fra	agme	nt			
					(c)			OTHE:										
			(ii	4)				URCE										
			\	-,	(E)			IVID			TE:							
			(iv	1		EDIA												
25			\	•	(C)			-						_				
25			-		(C) POS		CLO	NE:		Witi	nin l	Env	Gene	<del></del>				
25			(v)		POS	ITIO	CLO N IN	NB: GEN	OME:	With	nin Ex	Env pres	Gene ses	- ano	erve	d ant	ige:	nic
25			-		POS PRO	ITIO PERT	CLO N IN IES	ne: Gen Of S	OME:	With NCE:	in Ex	Env pres	Gene ses	- cons	erve	d ant	ige	nic
25			(v) (vi	)	POS PRO det	ITIO PERT ermi	CLO N IN IES nant	NE: GENO OF S	OME: EQUE	ICE:	in Ex	Env pres	Gene ses	 cons	erve	d ant	ige	nic
25 30			(v) (vi		POS PRO det	ITIO PERT ermi	CLO N IN IES nant	ne: Gen Of S	OME: EQUE	ICE:	in Ex	Env pres	Gene ses	 cons	erve	d ant	ige	nic
			(v) (vi	)	POS PRO det	ITIO PERT ermi	CLO N IN IES nant	NE: GENO OF S	OME: EQUE	ICE:	in Ex	Env pres	Gene ses	cons	erve	d ant	ige:	nic
	SEO	ID	(v) (vi	) ii)	POS PRO det SEQ	ITIO PERT ermi UENC	CLO N IN IES nant	NE: GENO OF S	OME: EQUE	ICE:	in Ex	Env pres	Gene ses	cons	erve	d ant	ige	nic
	SEQ	ID	(v) (vi	)	POS PRO det SEQ	ITIO PERT ermi UENC	CLO N IN IES nant	NE: GENO OF S	OME: EQUE	ICE:	in Ex	Env pres	Gene ses	cons	erve	d ant	ige:	nic
30	SEQ	ID	(v) (vi	) ii)	POS PRO det SEQ	ITIO PERT ermi UENC	CLO N IN IES nant	NE: GENO OF S	OME: EQUE	ICE:	in Ex	Env pres	Gene ses	cons			ige:	nic
	1		(v) (vi (vi NO:	) ii) EEE	POS PRO det SEQ 211-	ITIO PERT ermi UENC	CLO N IN IES nant E DE	NE: GENOF S	OME: EQUER	ICE:	Ex	pres	Bes ·	cons	15		ige:	nic
30	1 Cvs	Thr	(v) (vi (vi NO:	ii) EEE	POS PRO det SEQ 211-	ITIO PERT ermi UENC 2	CLO N IN IES nant E DE	NE: GENOF S	OME: EQUER PTION	ICE:	Ex	pres Ile	ses Ser	cons Leu	15 1 Gly		ige:	nic
30	1 Cvs	Thr	(v) (vi (vi NO:	ii) EEE	POS PRO det SEQ 211-	ITIO PERT ermi UENC 2	CLO N IN IES nant E DE	NE: GENOF S	OME: EQUER PTION	ICE:	Ex	pres Ile	ses Ser	cons Leu	15 1 Gly		ige:	nic
30	1 Cvs	Thr	(v) (vi (vi NO:	ii) EEE	POS PRO det SEQ 211-	ITIO PERT ermi UENC 2	CLO N IN IES nant E DE	NE: GENOF S	OME: EQUER PTION	ICE:	Ex	pres Ile	ses Ser	cons Leu	15		ige:	nic
<i>30</i>	1 Cvs	Thr	(v) (vi (vi NO:	ii) EEE	POS PRO det SEQ 211-	ITIO PERT ermi UENC 2	CLO N IN IES nant E DE	NE: GENOF S	OME: EQUER PTION	ICE: 10 Lys AAA	Ex	pres Ile	ses Ser	cons Leu	15 Gly GGA		ige	nic
30	1 Cys TGT	Thr ACA	(v) (vi (vi NO:	ii) EEE	POS PRO det SEQ 211- 5 Asn AAC	ITIO PERT ermi UENC 2	CLO N IN IES nant E DE	NE: GENOF S SCRI	OME: EQUER PTION Arg	ICE: I: 10 Lys AAA	Ex Ser AGT	Ile ATA	Ser TCT	Leu CTA	15 1 Gly 1 GGA		ige	nic
<i>30</i>	1 Cys TGT	Thr ACA	(v) (vi (vi NO:	ii) EEE	POS PRO det SEQ 211- 5 Asn AAC	ITIO PERT ermi UENC 2	CLO N IN IES nant E DE	NE: GENOF S SCRI	OME: EQUER PTION Arg AGA	ICE: I: 10 Lys AAA 25 Asp	Ser AGT	Ile ATA	Ser TCT	Leu CTA	15 Gly GGA 30		ige:	nic
<i>30</i>	1 Cys TGT	Thr ACA	(v) (vi (vi NO:	ii) EEE	POS PRO det SEQ 211- 5 Asn AAC	ITIO PERT ermi UENC 2	CLO N IN IES nant E DE	NE: GENOF S SCRI	OME: EQUER PTION Arg AGA	ICE: I: 10 Lys AAA 25 Asp	Ser AGT	Ile ATA	Ser TCT	Leu CTA	15 1 Gly 1 GGA		ige	nic
<i>30</i>	1 Cys TGT	Thr ACA	(v) (vi (vi NO:	ii) EEE	POS PRO det SEQ 211- 5 Asn AAC	ITIO PERT ermi UENC 2	CLO N IN IES nant E DE	NE: GENOF S SCRI	OME: EQUER PTION Arg AGA	ICE: I: 10 Lys AAA 25 Asp	Ser AGT	Ile ATA	Ser TCT	Leu CTA	15 Gly GGA 30		ige	nic
30 35 40	1 Cys TGT	Thr ACA	(v) (vi (vi NO:	ii) EEE	POS PRO det SEQ 211- 5 Asn AAC	ITIO PERT ermi UENC  2  Asn AAC	CLO N IN IES nant E DE	NE: GENOF S SCRI	OME: EQUER PTION Arg AGA	ICE: I: 10 Lys AAA 25 Asp	Ser AGT	Ile ATA	Ser TCT	Leu CTA	15 Gly GGA 30		ige	nic
<i>30</i>	1 Cys TGT Pro	Thr ACA G13 GG0	(v) (vi (vi NO:	ii) EEE ; Pro	POS PRO det SEQ 211- 5 Asn AAC	ITIO PERT ermi UENC  2  Asn AAC	CLO N IN IES nant E DE	NE: GENOF S SCRI	OME: EQUER PTION Arg AGA	ICE: I: 10 Lys AAA 25 Asp	Ser AGT	Ile ATA	Ser TCT	Leu CTA	15 Gly GGA 30		ige	nic
30 35 40	1 Cys TGT Pro CCA	The ACA	(v) (vi (vi NO: Arg	ii) EEE Pro	POS PRO det SEQ 211-5 Asn AAC 20 Ile ATI	ITIO PERT ermi UENC  2  Asn AAC	CLO N IN IES nant E DE	NE: GENOF S SCRI	OME: EQUER PTION Arg AGA	ICE: I: 10 Lys AAA 25 Asp	Ser AGT	Ile ATA	Ser TCT	Leu CTA	15 Gly GGA 30		ige	nic
30 35 40	1 Cys TGT Pro CCA	The ACA	(v) (vi (vi NO: Arg	ii) EEE ; Pro	POS PRO det SEQ 211-5 Asn AAC 20 Ile ATI	ITIO PERT ermi UENC  2  Asn AAC	CLO N IN IES nant E DE	NE: GENOF S SCRI	OME: EQUER PTION Arg AGA	ICE: I: 10 Lys AAA 25 Asp	Ser AGT	Ile ATA	Ser TCT	Leu CTA	15 Gly GGA 30		ige	nic

	(2)		INF	ORMA'	CION											
			(i)		SEQU	JENCI	E CHA	ARAC'	TER I	STICS	<b>S:</b>					
					(A)		LEN	GTH:	10	5						
					(B)		TYP	E: I	Nucle	eic A	Acid					
5					(C)		STR	ANDE	DNES	S: S	Singl	le				
					(D)			OLOG		Linea						
			(ii)	)					enom							
			(ii)	)		) (i			e or							
					(A)		•		E AS						-	
10					(B)		FRA	GMEN.	r Ty	PE:	Inte	ernal	Fra	agmer	ıt	
					(C)				rica:	_						
			(iii	i)		INA			: HIV							
					(E)				UAL :	ISOL	ATE:					
			(iv)	)		EDIA:		OURC	E:							
15					(C)		CLO					-		-		
			(v)						OME:							
			(vi)	)				OF S	RÓORI	ACE:	EXI	pres	ses (	conse	ervea	antigenic
					dete		-	oon T								
20			(V1:	ii)	SEQU	JENCI	e Dr	SCKI	PTIO	v:						
20																
	CEO	TD 3	ıo.	EE21	5.1											
	SEQ	זט נ	10:	EE2	13-1											
25	1				5					10					15	
		I1e	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Ser	I1e	His	Ile	G1y	
					AAC											
30					20					25					30	
					Phe											
	CCA	GGG	AGA	GCA	TTT	TAT	ACA	ACA	GGA	GAT	ATA	ATA	GGA	GAT	ATA	
35					35											
	_			His	•											
	AGA	CAA	GCG	CAT	TGT											
40	(0)		TME		PTON	EOD	CEO	TD 1	MO.	D D O 1 1	<b>.</b> .					
40	(2)			UKUTA.	CION											
			(i)		•	JENC:			TERI		<b>5</b> :					
					(A) (B)			GTH:	10! Nucl	_	A ~ 1 &					
					(C)				DNES		Sing.	ما				
45					(D)				Y:		•	16				
~			(ii	<b>)</b>		D• ~1	-		enom:							
			(11	,	V TIAI	J. C.	NIAN.	ro R	CITOIU	r¢ KI	447					

5		(ii) (iii) (iv) (v) (vi) (viii)	KIND (if peptide or protein):  (A) SEQUENCE ASSEMBLY METHOD: Overlap  (B) FRAGMENT TYPE: Internal Fragment  (C) HYPOTHETICAL:  ORIGINAL SOURCE: HIV  (E) INDIVIDUAL ISOLATE:  IMMEDIATE SOURCE:  (C) CLONE:  POSITION IN GENOME: Within Env Gene PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant  SEQUENCE DESCRIPTION:
15	SEQ ID	NO: EE2	15–2
	1		5 10 15
	l Cve Ile	Are Pro	Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly
20	TGT ATA	A AGA CCC	AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA
•			
			20 25 30
	D C1-	- Ama Ala	20 25 30 Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile
25	CCV CC	S VCV CCV	TIT TAT ACA ACA GGA GAT ATA ATA GGA GAT ATA
30	_	n Ala His A GCA CAT	
	(2)	TNFORMA	TION FOR SEQ ID NO: EE215-3
	(~)	(i)	SEQUENCE CHARACTERISTICS:
35			(A) LENGTH: 105
			(B) TYPE: Nucleic Acid
			(C) STRANDEDNESS: Single (D) TOPOLOGY: Linear
		(ii)	KIND: cDNA to genomic RNA
40		(ii)	KIND (if peptide or protein):
			(A) SEQUENCE ASSEMBLY METHOD: Overlap
			(B) FRACMENT TYPE: Internal Fragment
		()	(C) HYPOTHETICAL:
45		(iii)	ORIGINAL SOURCE: HIV (E) INDIVIDUAL ISOLATE:
		(iv)	IMMEDIATE SOURCE:
		\-·/	(C) CLONE:
		(v)	POSITION IN GENOME: Within Env Gene
50		(vi)	PROPERTIES OF SEQUENCE: Expresses conserved antigenic
50		/	determinant
		(viii)	SEQUENCE DESCRIPTION:

SEQ ID NO: EE215-3

50

55

5 10 1 5 Cys Ile Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly TGT ATA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA 25 10 20 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Thr Ile Ile Gly Asp Ile CCA GGG AGA GCA TIT TAT ACA ACA GGA ACA ATA ATA GGA GAT ATA 15 Arg Gln Ala His Cys AGA CAA GCA CAT TGT INFORMATION FOR SEQ ID NO: EEE217-1 20 (2) (i) SEQUENCE CHARACTERISTICS: LENGTH: 105 (A) (B) TYPE: Nucleic Acid STRANDEDNESS: Single (C) TOPOLOGY: Linear 25 (D) KIND: cDNA to genomic RNA (ii) KIND (if peptide or protein): (ii) SEQUENCE ASSEMBLY METHOD: Overlap (A) FRACMENT TYPE: Internal Fragment (B) HYPOTHETICAL: (C) 30 ORIGINAL SOURCE: HIV (iii) INDIVIDUAL ISOLATE: (E) IMMEDIATE SOURCE: (iv) CLONE: (C) POSITION IN GENOME: Within Env Gene (v) PROPERTIES OF SEQUENCE: Expresses conserved antigenic (vi) determinant SEQUENCE DESCRIPTION: (viii) 40 SEO ID NO: EEE217-1 10 Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Gly Ile Ser Ile Gly 45 TGT ACA AGA CCC AAC AAC AAT ACA AGA AGG GGT ATA AGT ATA GGA

Pro Gly Arg Ala Phe Val Tyr Ala Thr Lys Ile Ile Gly Asp Ile CCA GGG AGA GCA TTT GTT TAT GCA ACA AAA ATA ATA GGA GAT ATA Arg Gln Ala His Cys AGA CAA GCA CAT TGT 10 INFORMATION FOR SEQ ID NO: EE217-2 (2) SEQUENCE CHARACTERISTICS: (i) LENGTH: 105 (A) TYPE: Nucleic Acid (B) 15 STRANDEDNESS: Single (C) (D) TOPOLOGY: Linear (ii) KIND: cDNA to genomic RNA KIND (if peptide or protein): (ii) SEQUENCE ASSEMBLY METHOD: Overlap (A) 20 FRAGMENT TYPE: Internal Fragment (B) (C) HYPOTHETICAL: (iii) ORIGINAL SOURCE: HIV INDIVIDUAL ISOLATE: (iv) IMMEDIATE SOURCE: 25 CLONE: (v) POSITION IN GENOME: Within Env Gene (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant (viii) SEQUENCE DESCRIPTION: 30 SEQ ID NO: EE217-2 35 10 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly TGT ACA AGA CCC AAT AAC AAT ACA AGA AAA AGT ATA ACT ATA GGA 40 20 25 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA 45 35 Arg Gln Ala His Cys AGA CAA GCA CAT TGT 50

	(2)	INFORMA	TION FOR SEQ ID NO: EE228-1 SEQUENCE CHARACTERISTICS:
_		(-)	(A) LENGTH: 105
5			(B) TYPE: Nucleic Acid
			(C) STRANDEDNESS: Single (D) TOPOLOGY: Linear
		(ii)	KIND: cDNA to genomic RNA
		(ii)	KIND (if peptide or protein):
10			(A) SEQUENCE ASSEMBLY METHOD: Overlap
			(B) FRACMENT TYPE: Internal Fragment
		(	(C) HYPOTHETICAL:
		(iii)	ORIGINAL SOURCE: HIV (E) INDIVIDUAL ISOLATE:
15		(iv)	IMMEDIATE SOURCE:
		<b>\/</b>	(C) CLONE:
		(v)	POSITION IN GENOME: Within Env Gene
		(vi)	PROPERTIES OF SEQUENCE: Expresses conserved antigenic
20		(viii)	determinant SEQUENCE DESCRIPTION:
		(*****)	ondomica appoint from.
	SEQ ID	NO: EE2	28–1
25			
	1		5 10 15
			Asn Asn Asn Thr Arg Lys Ser Ile Pro Ile Gly
	TGT ACA	AGA CCC	AAC AAC AAT ACA AGA AAA AGT ATA CCT ATA GGA
30	•		
			20 25 30
			Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile
	CCA GGG	AGA GCA	TIT TAT ACA ACA GGA GAT ATA ATA GGA GAT ATA
35			
			35
	Arg Gln	Ala His	Cys
	AGA CAA	GCA CAT	TGT
40			
	(2)	INFORMA	TION FOR SEQ ID NO: EE228-2
	,	(i)	SEQUENCE CHARACTERISTICS:
			(A) LENGTH: 105
45			(B) TYPE: Nucleic Acid
~			(C) STRANDEDNESS: Single (D) TOPOLOGY: Linear
		(ii)	KIND: cDNA to genomic RNA
		• •	

5			(ii)		KINI (A) (B) (C)		SEQU FRAC HYPO	ence Ment Thet	ASS TYP CICAL	EMBL E: -	Y ME	: THOE ernal					
			(iii		ORIG		INDI	VIDU	JAL I		TE:				<del></del>		
			(iv)		(C)	EDIAT MOIT	CLON	E:		With	in I	Post (	lene	-			
10			(v) (vi)		PROF	ERTI Ermin	ES C	F SE	ATE: EQUEN	ICE:	Ехј	press	es (	conse	erved	antig	enic
			(vii	li)		JENCE		CRIE	PTION	i:							
15	SEQ	ID 1	10:	EE2	28–2												
	1				5					10					15		
20	Cve	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile	Pro	Ile	Gly		
	TGT	ACA	AGA	CCC	AAC	AAC	AAT	ACA	AGA	AAA	AGT	ATA	CCI	AIA	GGA		
					20					25					30		
25	Pro	Gly	Arg	Ala	Phe	Tyr	Thr	Thr	G1y	Asp	Ile	Ile	G1y	Авр	Ile		
	CCA	GGG	AGA	GCA	TTT	TAT	ACA	ACA	GGA	GAT	ATA	ATA	GGA	GAT	ATA		
	<b>A</b>	C1-	A1.a	Wi o	35 Cys												
30	AGA	CAA	GCA	CAT	TGT										•		
	(2)		INF	ORMA'	TION	FOR	SE0	ID I	NO:	EE22	8–3						
35	(2)		(i)		SEQ	UENC	E CH	ARAC'	TERI	STIC	S:						
30					(A)		LEN TYP	GTH:	10. Nucl	_	h.i.a					•	
					(B) (C)				DNES		Sing						
					(D)		TOP	OLOG	Y:	Line	ar						
40			(ii		KIN	D: c	DNA	to g	enom	ic R	NA						
70			(ii	)		D (i	f pe	ptid	e or	pro pro	tein	): ETHO	<b>D</b> •	Over	lan		
					(A) (B)		FRA	CMEN	T TY	PE:	Int	erna	l Fr	agme	nt		
					(c)				TICA								
45			(ii	i)	ORI	GINA											
45					(E)				UAL	ISOL	ATE:	_					
			(iv	7	(C)	EDIA		NE:	E.								
			(v)		POS	ITIC	N IN	GEN	OME:	Wit	hin	Env	Gene	:			
50	•		(vi		PRO	PERT	IES	OF S	EQUE	NCE:	Ex	tpres	ses	cons	erved	l anti	genic
50			(	ii)		ermi OUENC			יזיים	N•							
			(V)	.11/	2E/	COMM	i DE	NOCK 1		44 .							

SEQ ID NO: EE228-3 5 5 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Pro Ile Gly TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CCT ATA GGA 30 20 10 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile CCA GGG AGA GCA TTT TAT ACA ACA GGA GAT ATA ATA GGA GAT ATA 35 15 Arg Gln Ala His Cys AGA CAA GCA CAT TGT INFORMATION FOR SEQ ID NO: EE229-1 (2) 20 SEQUENCE CHARACTERISTICS: (i) LENGTH: 102 (A) TYPE: Nucleic Acid (B) STRANDEDNESS: Single (C) TOPOLOGY: Linear (D) 25 KIND: cDNA to genomic RNA (ii) KIND (if peptide or protein): (ii) SEQUENCE ASSEMBLY METHOD: Overlap (A) (B) FRAGMENT TYPE: Internal Fragment HYPOTHETICAL: (C) 30 ORIGINAL SOURCE: HIV (iii) INDIVIDUAL ISOLATE: (iv) IMMEDIATE SOURCE: CLONE: POSITION IN GENOME: Within Env Gene (v) 35 PROPERTIES OF SEQUENCE: Expresses conserved antigenic (vi) determinant SEQUENCE DESCRIPTION: (viii) SEO ID NO: EE229-1

66

Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Ser Ile His Ile Gly

TGT ACA AGA CCC AAT AAC AAT ACA AGA AGA AGT ATA CAT ATA GGA

45

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					20					25					30			
	Pro	G1y	Arg	Ala	Phe	Tyr	Ala	Thr	Asp	Ile	Ile	Gly	Asn	Ile	Arg			
	CCA	GGG	AGA	GCA	TTT	TAT	GCA	ACA	GAT	ATA	ATA	GGA	AAT	ATA	AGA			
5																		
				_	35													
		Ala		-														
	ÇAA	GCA	CAT	161														
10																		
	(2)		TNF	)RMA	TON	FOR	SEO	TD I	NO: 1	3E229	9-2							
	(2)		(i)	/14 M 1 /					CER IS									
			(-/		(A)			GTH:	10:									
					(B)				Nucle	eic A	Acid							
15					(C)		STRA	ANDEI	DNES	S: S	Sing:	le						
					(D)		TOP	DLOG	r: 1	Line	ar			•				
			(ii)	)					enom:									
			(ii)	)		) (ii			e or						_			
20					(A)				E ASS									
					(B)				TYI		Int	erna.	Fra	gme	ıt			
					(C)				CICA	_								
			( <b>ii</b> :	L)		FINAL			HIV		\TP.							
			(iv	`	(E)	71\ T A 1		DURC	JAL I	raora	ALE:						-	
25			(10	,	(C)	MIM.	CLO		<b>.</b>									
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			()		DUC.	TTO	MT I	CEN	WF.	W4+1	dn 1	Rnv (	ene					
			(v)						ME:						erved	ant	igen:	ic
			(v) (vi		PRO	PERT	IES (								erved	ant	igen	ic
			iv)	)	PROI	PERT:	IES ( nant	OF SI	EQUEI	VCE:					erved	ant	igen:	ic
30			iv)	)	PROI	PERT:	IES ( nant	OF SI		VCE:					erved	ant	igen:	ic
30			iv)	)	PROI	PERT:	IES ( nant	OF SI	EQUEI	VCE:					erved	ant	igen:	ic
30	SEQ	IĎ I	(vi)	)	PROI dete SEQU	PERT:	IES ( nant	OF SI	EQUEI	VCE:					erved	ant	igen	ic
<b>30</b>	SEQ	IĎ l	(vi)	ii)	PROI dete SEQU	PERT:	IES ( nant	OF SI	EQUEI	VCE:					erved	ant	igen	lc
30		IĎ l	(vi)	ii)	PROI dete SEQU	PERT:	IES ( nant	OF SI	EQUEI	VCE:						ant	igen:	ic
	1		(vi) (vi) (vi)	ii) EE2:	PROD dete SEQU 29-2	PERT: ermin JENCI	IES ( nant E DE	OF SI	EQUEI PTIOI	NCE:	Ex	pres	3e8 (	conse	15	ant	igen	ic
	1 Сув	Thr	(vi:	ii) EE2: Pro	PROD dete SEQU 29-2 5 Gly	PERT: ermin JENC! Asn	IES ( nant E DE:	OF SI	EQUEI PTIOI Arg	NCE: N: 10 Lys	Ex:	pres:	His	Ile	15 Gly	ant	igen	ic
	1 Сув	Thr	(vi:	ii) EE2: Pro	PROD dete SEQU 29-2 5 Gly	PERT: ermin JENC! Asn	IES ( nant E DE:	OF SI	EQUEI PTIOI	NCE: N: 10 Lys	Ex:	pres:	His	Ile	15 Gly	ant	igen:	Lc
	1 Сув	Thr	(vi:	ii) EE2: Pro	PROD dete SEQU 29-2 5 Gly	PERT: ermin JENC! Asn	IES ( nant E DE:	OF SI	EQUEI PTIOI Arg	NCE: N: 10 Lys	Ex:	pres:	His	Ile	15 Gly	ant	igen:	Lc
	1 Сув	Thr	(vi:	ii) EE2: Pro	PROI dete SEQU 29-2 5 Gly GGC	PERT: ermin JENC! Asn	IES ( nant E DE:	OF SI	EQUEI PTIOI Arg	NCE: N: 10 Lys	Ex:	pres:	His	Ile	15 Gly	ant	igen:	ic
35	1 Cys TGT	Thr ACA	(vi) (vi) NO: Arg AGA	Pro	PROI dete SEQU 29-2 5 Gly GGC	PERT: PERMIN JENCI ASR AAC	IES (nant nant E DE:	Thr ACA	Arg AGA	IO Lys AAA	G1y GGT	Ile ATA	His CAT	Ile ATA	15 Gly GGA	ant	igen:	ic
35	1 Cys TGT	Thr ACA	(vi) (vi) NO: Arg AGA	) ii) EE2: Pro CCC	PROD dete SEQUE 29-2 5 Gly GGC 20 Ile	PERT: PERC! JENC! Asn AAC	Asn AAT	Thr ACA	Arg AGA	IO Lys AAA 25 Ile	Gly GGT	Ile ATA	His CAT	Ile ATA	15 Gly GGA 30 Arg	ant	igen:	Lc
35	1 Cys TGT	Thr ACA	(vi) (vi) NO: Arg AGA	) ii) EE2: Pro CCC	PROD dete SEQUE 29-2 5 Gly GGC 20 Ile	PERT: PERC! JENC! Asn AAC	Asn AAT	Thr ACA	Arg AGA	IO Lys AAA 25 Ile	Gly GGT	Ile ATA	His CAT	Ile ATA	15 Gly GGA 30 Arg	ant	igen:	Ic
35 40	1 Cys TGT	Thr ACA	(vi) (vi) NO: Arg AGA	) ii) EE2: Pro CCC	PROD dete SEQUE 29-2 5 Gly GGC 20 Ile	PERT: PERC! JENC! Asn AAC	Asn AAT	Thr ACA	Arg AGA	IO Lys AAA 25 Ile	Gly GGT	Ile ATA	His CAT	Ile ATA	15 Gly GGA 30 Arg	ant	igen:	ic
35	1 Cys TGT	Thr ACA	(vi) (vi) NO: Arg AGA	) ii) EE2: Pro CCC	PROD dete SEQUE 29-2 5 Gly GGC 20 Ile	PERT: PERC! JENC! Asn AAC	Asn AAT	Thr ACA	Arg AGA	IO Lys AAA 25 Ile	Gly GGT	Ile ATA	His CAT	Ile ATA	15 Gly GGA 30 Arg	ant	igen:	ic
35 40	1 Cys TGT Pro	Thr ACA	(vi: (vi: NO: Arg AGA	ii) EE2: Pro CCC	PROI dete SEQUE 29-2 5 Gly GGC 20 Ile ATT	PERT: PERC! JENC! Asn AAC	Asn AAT	Thr ACA	Arg AGA	IO Lys AAA 25 Ile	Gly GGT	Ile ATA	His CAT	Ile ATA	15 Gly GGA 30 Arg	ant	igen:	Lc
35 40	1 Cys TGT Pro CCA	Thr ACA Gly GGG	(vi: (vi: NO: Arg AGA Arg AGA	Pro CCC	PROI dete SEQUE 29-2 5 Gly GGC 20 Ile ATT	PERT: PERC! JENC! Asn AAC	Asn AAT	Thr ACA	Arg AGA	IO Lys AAA 25 Ile	Gly GGT	Ile ATA	His CAT	Ile ATA	15 Gly GGA 30 Arg	ant	igen:	Lc

٠;	(2)	INFORMA	TION FOR SEQ ID NO: EE229-3
٠.		(i)	SEQUENCE CHARACTERISTICS:
			(A) LENGTH: 102
_			(B) TYPE: Nucleic Acid
5			(C) STRANDEDNESS: Single
			(D) TOPOLOGY: Linear
٠.		(ii)	KIND: cDNA to genomic RNA
		(ii)	KIND (if peptide or protein):
			(A) SEQUENCE ASSEMBLY METHOD: Overlap
10			(B) FRAGMENT TYPE: Internal Fragment
			(C) HYPOTHETICAL:
		(iii)	ORIGINAL SOURCE: HIV
			(E) INDIVIDUAL ISOLATE:
		(iv)	IMMEDIATE SOURCE:
15			(C) CLONE:
		(v)	POSITION IN GENOME: Within Env Gene
		(vi)	PROPERTIES OF SEQUENCE: Expresses conserved antigenic
			determinant
20		(viii)	SEQUENCE DESCRIPTION:
20			
•			
	SEQ ID	NO: EE2	29–3
			•
25	•		r 10 15
	1 _		5 10 15
			Gly Asn Asn Thr Arg Lys Gly Ile His Ile Gly
	TGT ACA	AGA CCC	GGC AAC AAT ACA AGA AAA GGT ATA CAT ATA GGA
		-	
30			20 25 30
•	Pro Clr	. 420 410	Ile Tyr Ala Thr Asp Ile Ile Gly Asp Ile Arg
	•	_	ATT TAT GCA ACA GAT ATA ATA GGA GAT ATA AGA
	CON GGG	non our	All the our non our ain ain our our ain non
35			. 35
	Gin Ala	His Cys	
		CAT TGT	
	<u> </u>		
40	(2)	INFORMA	TION FOR SEQ ID NO: EEE244-1
	<b>\</b> -,	(i)	SEQUENCE CHARACTERISTICS:
			(A) LENGTH: 102
			(B) TYPE: Nucleic Acid
			(C) STRANDEDNESS: Single
45			(D) TOPOLOGY: Linear
	ī	(ii)	KIND: cDNA to genomic RNA
3			-

5			(ii) (iii) (iv) (v) (vi) (vii	i)	(A) (B) (C) ORIC (E) IMMI (C) POSI	IANIS LAIGS	SEQUENT SEQUEN	JENCI GMENT OTHET JRCE IVIDI OURCI VE: GENCOF SI	E AS: I TYI IICAI : HIV UAL : E: OME:	SEMBI PE: L: V ISOLA With	Inte	Env (	l Fra		nt	antigenic
15	SEQ I	D N	0:	EE24	4-1											
					5					10					15	
00	1 Cys T	hr	A == a	Pro	-	Aon	Agn	T1e	l.ve		Aro	Ser	Tle	Hie		
20	TGT A															
										0.5					20	
	Gly P		C1 w	A=~	20 Pro	Pho	Ture	The	The	25	T1a	C1 w	Acn	Tla	30	
25	GGA C															
<i>30</i>	Gln A CAA G		_	-	35											
	(2)		TNIE/	NDMA"	PTON	FOB	CPA	TD I		2E91.1						
	(2)		INFORMATION FOR SEQ ID NO: EE244-2 (i) SEQUENCE CHARACTERISTICS:													
35			\ <b>-</b> /		(A)			STH:			•					
					(B)		TYPI	Z: 1	Vucle	eic #	Acid					
					(C)					S: S	_	le				
			(ii)		(D)	): cI		DLOG		Linea						
40			(11)			) (ii						):				
					(A)			-		-	LY MI	ETHOI		Over		
					(B)			MEN.			Inte	ernal	l Fra	agmer	at	
			(iii		(C)	INAI		THE:								
45			(11)	. ,	(E)	TIANT				, ISOL#	ATE:					
			(iv)	)		CAIC										<del></del>
					(C)		CLO							-		
			(v)									Env (			-	
50			(vi)	,		ERTI Ermic		JF SI	<b>SQUET</b>	WCE:	Exp	pres	ses (	conse	erved	antigenic
			(vii	ii)		ENCE		SCRII	PTIO	<b>1</b> :						

SEQ ID NO: EE244-2 10 Cys Thr Arg Pro Asn Asn Asn Ile Lys Ile Arg Ser Ile His Ile TGT ACA AGG CCC AAC AAC AAT ATA AAA ATA AGA AGT ATA CAT ATA 20 25 30 10 Gly Pro Gly Arg Pro Phe Tyr Thr Thr Lys Ile Gly Asp Ile Arg GGA CCA GGG AGA CCA TTT TAT ACA ACA AAA ATA GGA GAT ATA AGA 35 15 Gln Ala Tyr Cys CAA GCA TAT TGT (2) INFORMATION FOR SEQ ID NO: EE244-3 20 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 102 (B) TYPE: Nucleic Acid STRANDEDNESS: Single (C) TOPOLOGY: Linear (D) 25 KIND: cDNA to genomic RNA (ii) KIND (if peptide or protein): (ii) SEQUENCE ASSEMBLY METHOD: Overlap (A) FRACMENT TYPE: Internal Fragment (B) (C) HYPOTHETICAL: 30 (iii) ORIGINAL SOURCE: HIV INDIVIDUAL ISOLATE: (E) (iv) IMMEDIATE SOURCE: CLONE: (v) POSITION IN GENOME: Within Env Gene PROPERTIES OF SEQUENCE: Expresses conserved antigenic (vi) determinant (viii) SEQUENCE DESCRIPTION: SEQ ID NO: EE244-3 10

45

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Cys Thr Arg Pro Asn Asn Asn Ile Lys Ile Arg Ser Ile His Ile

TGT ACA AGG CCC AAC AAC AAT ATA AAA ATA AGA AGT ATA CAT ATA

					20					25					30	
	G1y	Pro	Gly	Arg	Pro	Phe	Tyr	Thr	Thr	Lys	Ile	G1y	Asp	Ile	Arg	
	GGA	CCA	GGG	AGA	CCA	TTT	TAT	ACA	ACA	AAA	ATA	GGA	GAT	ATA	AGA	
5																
			_	_	35											
		Ala														
	UAA	GCA	IAI	161												
10																
	(2)		INF	ORMA'	TON	FOR	SEO	ID I	NO: 1	EE289	9-1					
	\-/		(i)					ARAC'								
			•		(A)			GTH:	10							
					(B)		TYP	E: 1	Nucle	eic A	Acid					
15					(C)			ANDE		S: S	Sing	le				
					(D)	_		OLOG		Linea						
			(ii					to g								
			(ii	)		0 (1:		ptid					n. 1	<b>~</b>	1	
20					(A) (B)		•	UENC! GMEN:				erna.				
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			( <b>ii</b> :	i )		GINA		URCE								
			,	-,	(E)			IVID			ATE:					
			(iv	)	IMM	EDIA:	re s	OURC	E:							
25					(C)		CLO							_		
			(v)					GEN								
			(vi	)				OF S	EQUE	MCE:	Ex	pres	ses (	cons	erved	l antigenic
			<i>(</i>			ermi		COD T	DTT ()	NT -						
30			(V1	ii)	SEQ	OFTAC	e De	SCRI	LIIUI	N :						
	SE0	ID 1	NO:	EE2	89-1											
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35	1				5					10					15	
															G1y	
	TGT	ACA	AGA	ccc	AAC	AAC	AAT	ACA	AGA	AAA	GGT	ATA	CAT	ATA	GGA	
40					20					25					30	
	Pro	G1 v	Arg	Ala		Tvr	Thr	Thr	G1v		Ile	I1e	G1v	Asp		
		•	_			-		ACA			. — .					
45																
45					35											
	_			His	-											
	AGA	CAA	GCA	CAT	TGT											
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50																

	(2)	INFORMA.	TION FOR SEQ ID NO: EE289-2
		(i)	SEQUENCE CHARACTERISTICS:
5			(A) LENGTH: 105
3			(B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single
		(ii)	(D) TOPOLOGY: Linear KIND: cDNA to genomic RNA
		(ii)	KIND (if peptide or protein):
10		(11)	(A) SEQUENCE ASSEMBLY METHOD: Overlap
			(B) FRACMENT TYPE: Internal Fragment
			(C) HYPOTHETICAL:
		(iii)	ORIGINAL SOURCE: HIV
			(E) INDIVIDUAL ISOLATE:
15		(iv)	IMMEDIATE SOURCE:
			(C) CLONE:
		(v)	POSITION IN GENOME: Within Env Gene
		(vi)	PROPERTIES OF SEQUENCE: Expresses conserved antigenic
20			determinant
		(V111 <i>)</i>	SEQUENCE DESCRIPTION:
	SEQ ID	NO: EE2	89–2
	•		
25			
	1		5 10 15
	Cys Thr	Arg Pro	Asn Asn Asn Thr Arg Lys Gly Ile His Ile Gly
	TGT ACA	AGA CCC	AAC AAC AAT ACA AGA AAA GGT ATA CAT ATA GGA
30			•
			20 25 30
	Pro Cly	Aro Ala	Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asp Ile
	CCA GGG	AGA GCA	TIT TAT ACT ACA GGA GAA ATA ATA GGA GAT ATA
35			
			35
	_	Ala His	
	AGA CAA	GCA CAT	TGT
40			
40	(0)	T31507344	MYON BOD OBO ID NO. EPROO 1
	(2)		TION FOR SEQ ID NO: EE290-1
		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 105
			(B) TYPE: Nucleic Acid
45			(C) STRANDEDNESS: Single
-			(D) TOPOLOGY: Linear
		(ii)	KIND: cDNA to genomic RNA
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			(ii	)	(A) (B)		SEQ FRA	GMEN:	E AS	SEMBI PE:	LY M	ETHO:		Over:	_	
5			(ii	i)	(C) ORIC (E)	SINA	L SO!	OTHE: URCE IVIDI	: HI	7	ATE:					
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10			(v) (vi		PROI		IES (	GENO OF SI							erved	antigenic
			(vi	ii)		-		SCRI	PTIO	¥:						
15	SEQ	ID I	NO:	EE2	90–1											
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20														Leu		
	TGT	ACA	AGA	CCC	AAC	AAC	AAT	ACA	AGA	AAA	AGT	ATA	CAT	CTA	GGG	
					20					25					30	
25														Asp GAT		
	UCA	666	AUA	GUA		·	nun	,	GGA	GAC	nin	VIW	GGA	GNI	NIU	
•	Aro	G1n	Ala	His	35 Cvs											
30				CAT												•
	(2)		INF(	ORMA?				ID I								
35			(1)		(A)	) EIVO	LEN		10:		•					
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					(D)			DLOG				.6				
40			(ii)					to ge				١.				
			(ii	,	(V)	) (11		DENCI					D: (	Over	lap	
					(B) (C)			MENT OTHE			Int	erna.	l Fra	agme	nt	
			(iii	L)		INAI		URCE:	-	_						
45			<i>(:</i>		(E)			IVID		SOL	ATE:					<del> </del>
			(iv	,	(C)	MTW.	CLOI	DURCI NE :						<u>-</u>		
			(v)					GEN							_	
50			(vi	,		PERT: ermi:		of Si	eQUEI	NCE:	Ext	pres	ses (	cons	erved	antigenic
			(vi	li)				SCRI	PTIO	V:						

SEQ ID NO: EE293-1

5	1 Cys TGT	Thr ACA	Arg AGA	Pro CCC	5 Asn AAC	Asn AAC	Asn AAT	Thr ACA	Arg AGA	10 Lys AAA	Ser AGT	Ile ATA	His CAT	Ile ATA	15 Gly GGA		
10	Pro CCA	G1y GGG	Arg AGA	Ala GCA	20 Phe TTT	Tyr TAT	Thr ACA	Thr ACA	G1y GGA	25 Glu GAA	Ile ATA	Ile ATA	G1y GGA	Asn AAT	30 Ile ATA		
15			Ala GCA				•										
20	(2)		INF(	ORMA'	(A) (B) (C)		LENG TYPI STR	ARAC' GTH: E: :	TERI 10 Nucl DNES	STIC: 5 eic <i>i</i> S: :	S: Acid Sing	le					
<b>25</b>			(ii (ii	•	(A) (B)		DNA f pe SEQ FRA	to g ptid UENC GMEN	T TY	ic RI prof SEMBI PE:	NA tein LY M	ETHO:	D: (				
30			(ii	)	(E) IMM (C)	EDIA'	L SO IND IE SO CLO	URCE IVID OURC NE:		V ISOL							
35			(v) (vi (vi		PRO det	PERT: e <b>rmi</b> :	IES ( nant	OF S		NCE:			Gene ses		erved	anti	genic
40	SEQ	ID 1	NO:	EE2	93–2												
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Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

				•	20					25					30				
	D	C1	A ===	Δ1 a	Dho	Tvr	Thr	Thr	G1v	G1u	Ile	I1e	G1y	Asn	Ile	:			
	PIO	GIA	VCV WTR	CCV	Julul	TAT	ACA	ACA	GGA	GAA	ATA	ATA	GGA	AAT	ATA	1			
	CUA	GGG	MGM	GUM	111	7117													
5																			
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	Arg	GIn	Ala	HIS	Cys														
	AGA	CAA	GCA	CAT	IGI														
10																			
,,						EOD	CEO	TD	NO.	FF2Q3	<b>3</b> _3								
	(2)			OKMA:	LION	XU1	yaç To T	$\Delta D \Delta C$	TEDT	EE293 STICS									
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					(B)		TIP	E:	MICT	GIC Y	otae actu	1.							
15					(C)		STR	ANUL	ar Tineo	S: S	orn8	16							
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			(ii		KIN	D: c	DNA	to 8	enom	ic R	MA Nata	١.							
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20					(B)					PE:	mu	erne	LI FA	agm	311 0				
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25					(C)		CLC	NE:						_					
			(v)	)	POS	ITIC	II NC	1 GEI	NOME:	Wit	nın	Env	Gen	=		.ad	ant i	een i	c
			iv)	.)	PRO	PER'	ries	OF :	SEQUE	NCE:	ES	pre	sses	COII	BGT A	Eu	an	P	_
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			tv)	lii)	SEC	UEN(	CE D	ESCR	IPT10	)N:			• .						
30																			
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35	1				5					10				-1		15			
	Cvs	Th	r Arg	g Pro	Ast	Ası	n As	n Th	r Ar	g Lys	s Se	r II	е на	8 II	e G	Ly			
,	TGT	' AC	A AG	A CC	C AAC	AA C	C AA	T AC	A AG	A AAA	A AG	T AT	A CA	T AI	A G	<i>i</i> Α			
40					20	)				2.	5					30			
	Pro	G1	v Ar	R Al	a Pho	e Ty	r Th	r Th	r Gl	y Glu	1 II	e Il	e Gl	y As	n I.	le			
	CCA	GG	G AG	A GC	A TT	ΓΙΑ	T AC	A AC	A GG	A GA	A AT	TA A	A GG	A A	AT A	TA			
45					3	5													
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	VC.	7 LV	A CC	A CA	T TG	T													
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	(2)		INF(	)RMA]				ARAC'		EE295 STICS						
					(B)		TYP			; eic <i>l</i>	Acid					
5					(c)				DNES		Sing	le				
					(D)		TOP	DLOG	Y: 1	Linea	ar					
			(ii)	)						ic Ri						
			(ii)	)		(i)				prot						
10					(A)		-						):_ (			
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					(C)				rical							
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			(iv)		(E)	DIA				ISOL/	TIE:					<del></del>
15			(IV)	,	(C)	MIU.	CLO		•							
			(v)			TION			OME:	With	nin l	Env (	Gene	-		
			(vi)											conse	erved	antigenic
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			(vi	ii)	SEQU	JENCI	DE	SCRI	PTIO	: 1						
20																
	SEQ	ID N	10:	EE29	95–1											
25	1				5					10					15	
	Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	G1y	Ile	His	Ile	Gly	
	TGT	ACA	AGA	CCC	AAC	AAC	AAT	ACA	AGA	AAA	GGT	ATA	CAT	ATA	GGA	
30									•	05					20	
,	n	O1	A	A1 -	20	T	A1 -	Th	T	25	T1.	T1.	C1	A ==	30	
													Gly GGA			
	CUA	GGG	nun	GUA	111	IVI	GUA	מטמ	nnn	GAC	AIN	VIV	GOL	GZII	AIA	
35					35											
	Arg	G1n	Ala	His	Cys											
	AGA	CAA	GCA	CAT	TGT											
40	(2)		INF	ORMA'	CION	FOR	SEO	ID 1	NO:	EE29!	5-2					
			(i)				•			STIC					•	
					(A)			GTH:	10							
					(B)		TYP	E: 1	Nucl	eic A	Acid					
					(C)		STR	ANDE	DNES	S: :	Sing	1e				
45					(D)					Line						
			(ii	)	KIN	D: cl	DNA	to g	enom	ic R	NA					

		(ii)	KIND (if peptide or protein):  (A) SEQUENCE ASSEMBLY METHOD: Overlap  (B) FRACMENT TYPE: Internal Fragment  (C) HYPOTHETICAL:
5		(iii)	ORIGINAL SOURCE: HIV (E) INDIVIDUAL ISOLATE:
		(iv)	IMMEDIATE SOURCE:
10		(v) (vi)	POSITION IN GENOME: Within Env Gene PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
		(viii)	SEQUENCE DESCRIPTION:
15	SEQ II	O NO: EE	295–2
	•		5 10 15
	1 Cvs T	hr Arg Pi	o Asn Asn Asn Thr Arg Lys Gly Ile His Ile Gly
20	TGT A	CA AGA CO	C AAC AAC AAT ACA AGA AAA GGT ATA CAT ATA GGA
			20 25 30
	Pro C	1 w Ara A'	to the Tyr Ale Thr Lys Asp Ile Ile Gly Asp Ile
25	CCA G	GG AGA G	CA TIT TAT GCA ACA AAA GAC ATA ATA GGA GAT ATA
			35
30	Arg G AGA C	ln Ala H AA GCA C	is Cys AT TGT
	(2)		MATION FOR SEQ ID NO: EE297-1
35		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 105
			(B) TYPE: Nucleic Acid
			(C) STRANDEDNESS: Single
			(D) TOPOLOGY: Linear KIND: cDNA to genomic RNA
40		(ii) (ii)	KIND: CLMA to genomic Ada KIND (if peptide or protein):
		(11)	(A) SEQUENCE ASSEMBLY METHOD: Overlap
	-		(B) FRAGMENT TYPE: Internal Fragment
			(C) HYPOTHETICAL:
45		(iii)	
		(iv)	(E) INDIVIDUAL ISOLATE:
			(C) CLONE:
		(v)	POSITION IN GENOME: Within Env Gene
50		(vi)	
		(vii:	determinant i) SEQUENCE DESCRIPTION:

SEQ ID NO: EE297-1 5 10 5 Cys Ile Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Asn Ile Gly TGT ATA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA AAT ATA GGA 30 25 20 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asn Ile 10 CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA AAT ATA 15 Arg Gln Ala His Cys AGA CAA GCA CAT TGT INFORMATION FOR SEQ ID NO: EE297-2 (2) SEQUENCE CHARACTERISTICS: 20 (i) (A) LENGTH: 105 (B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single (D) TOPOLOGY: Linear KIND: cDNA to genomic RNA (ii) (ii) KIND (if peptide or protein): (A) SEQUENCE ASSEMBLY METHOD: Overlap FRAGMENT TYPE: Internal Fragment (B) (C) HYPOTHETICAL: (iii) ORIGINAL SOURCE: HIV 30 INDIVIDUAL ISOLATE: (E) (iv) IMMEDIATE SOURCE: (C) CLONE: (v) POSITION IN GENOME: Within Env Gene PROPERTIES OF SEQUENCE: Expresses conserved antigenic 35 (vi) determinant (viii) SEQUENCE DESCRIPTION: SEQ ID NO: EE297-2

1 5 10 15

Cys Ile Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Asn Ile Gly

TGT ATA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA AAT ATA GGA

					20					25					30	
	Pro	G1y	Arg	Ala	Phe	Tyr	Thr	Thr	G1y	G1u	Ile	Ile	Gly	Asn	Ile	
	CCA	GGG	AGA	GCA	TTT	TAT	ACA	ACA	GGA	GAA	ATA	ATA	GGA	AAT	ATA	
5																
•					25											
	A	C1-	A1.	W	35											
				His CAT												
	non	OLMI	00.	0111	101											
10																
	(2)		INF	ORMA:	LION	FOR	SEQ	ID 1	NO: 1	EE29	7–3					
			(i)			JENC		ARAC:			3:					
					(A)			GTH:	10:							
15					(B)			e: i Andei				l a				
					(D)			OLOG		Line	_	re				
			(ii	)				to go								
			(ii					ptide				):				
20					(A)			UENCI								
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25			•	•	(C)		CLO	NE:						_		
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-	Arg	Gln	Ala	His	Cys											
	AGA	CAA	GCA	CAT	TGT											
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	(2)			)KMA					NO: 1									
			(i)			IRNCI			TER IS		<b>)</b> :							
_					(A)			GTH:										
5					(B)		TYP		Nuc1e			_						
					(C)				DNES		Sing	le		,				
					(D)		TOP	OLOG	Y: 1	Linea	ar							
			(ii)	)	KINI	): cl	DNA (	to go	enomi	ic Ri	<b>NA</b>							
			(ii)	)	KINI	(ii	E pe	ptid	e or	prot	tein	<b>)</b> :						
10					(A)		SEQ	JENC	E ASS	SEMBI	LY MI	CHOITS	): (	)ver	lap			
					(B)		FRA	MEN:	r TY	PE:	Inte	erna.	Fra	agmer	ıt			
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20			(vii	4)				SCR TI	PTIO	<b>1</b> •							:	
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	ord I	<i>D</i> 10	٠.	ادمن	/ <b>-</b> -1													
25																		
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	Cys T	L	<b></b>	D	-	A	A	Th.	A		C	T1.	A	T1.				
	TGT A																	
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	CCA G	، خاخا	AGA	GCA	TIT	TAT	AUA	ACA	GGA	GAA	AIA	AIA	GGA	GAI	AIA			
O.E																		
35					25													
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,	Arg G				•													
	AGA C	AA	GCA	CAT	TGT													
40																		
	(2)			)RMA'			_		NO: 1									
			(i)			JENC!			TERI		S:							
					(A)		LEN	GTH:	10	5								
					(B)		TYP	E: ]	Nucl	eic A	Acid							
45					(C)		STR	ANDE	DNES	S: S	Sing	le						
					(D)		TOP	OLOG	Y: 1	Line	ar							
			(ii)	)	KIN	D: c	DNA	to g	enom	ic R	AN							
								_										

5		(ii)	KIND (if peptide or protein): (A) SEQUENCE ASSEMBLY METHOD: Overlap (B) FRAGMENT TYPE: Internal Fragment (C) HYPOTHETICAL:
		(iii)	ORIGINAL SOURCE: HIV
		(1)	(E) INDIVIDUAL ISOLATE:
		(iv)	IMMEDIATE SOURCE: (C) CLONE:
10 .		(v)	POSITION IN GENOME: Within Env Gene
		(vi)	PROPERTIES OF SEQUENCE: Expresses conserved antigenic
			determinant
		(viii)	SEQUENCE DESCRIPTION:
15	SEO ID	NO: EE3	04-2
	55Q 12	223	- · -
	1	. A D	5 10 15
20			Asn Asn Asn Thr Arg Arg Ser Ile Asn Ile Gly AAC AAC AAT ACA AGG AGA AGT ATA AAT ATA GGA
	, IGI AG	AGA CCC	and mo mit that too trait that the term of
			20 25 30
25	Pro Gly	y Arg Ala	Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asp Ile
	CCA GG	3 AGA GUA	TTT TAT ACA ACA GGA GAA ATA ATA GGA GAT ATA
			35
30		n Ala His	
	AGA CAA	A GCA CAT	TGT
	(2)	INFORMA	TION FOR SEQ ID NO: EE304-3
35		. (i)	SEQUENCE CHARACTERISTICS:
		•	(A) LENGTH: 105
			(B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single
			(D) TOPOLOGY: Linear
40		(ii)	KIND: cDNA to genomic RNA
<b>40</b>		(ii)	KIND (if peptide or protein):
			(A) SEQUENCE ASSEMBLY METHOD: Overlap
•			(B) FRACMENT TYPE: Internal Fragment
		(iii)	(C) HYPOTHETICAL:
45		(111)	(E) INDIVIDUAL ISOLATE:
		(iv)	IMMEDIATE SOURCE:
			(C) CLONE:
		(v)	POSITION IN GENOME: Within Env Gene
50		(vi)	PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
	1	(viii)	
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SEQ ID NO: EE304-3

5									Ile ATA	
o									Asp GAT	
5	-		His CAT	-						

	(2) INFORMATION FOR SEQ ID NO: EE308-1 (i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 105
	(B) TYPE: Nucleic Acid
5	(C) STRANDEDNESS: Single
	(D) TOPOLOGY: Linear
	(ii) KIND: cDNA to genomic RNA
	(ii) KIND (if peptide or protein):
	(A) SEQUENCE ASSEMBLY METHOD: Overlap
10	(B) FRAGMENT TYPE: Internal Fragment
•	(C) HYPOTHETICAL:
	(iii) ORIGINAL SOURCE: HIV
	(E) INDIVIDUAL
15	ISOLATE:
75	(iv) IMMEDIATE SOURCE: (C) CLONE:
	(v) POSITION IN GENOME: Within Env Gene
	(vi) PROPERTIES OF SEQUENCE: Expresses conserved
	antigenic determinant
20	(viii) SEQUENCE DESCRIPTION:
	·/
	SEQ ID NO: EE308-1
25	1 5 10 15
	Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA
	TGT ACA AGA CCC AAC AAC AAI ACA AGA AGA AGA AGI AIM GAI AGA
30	
	20 25 30
	Pro Cly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asp Ile
	CCA GGC AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA GAT ATA
35	
	35
	Arg Gln Ala His Cys
	AGA CAA GCA CAT TGT
40	
	(2) INFORMATION FOR SEQ ID NO: EE308-2
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105
•	(B) TYPE: Nucleic Acid
45	(C) STRANDEDNESS: Single
	(D) TOPOLOGY: Linear
	(ii) KIND: cDNA to genomic RNA
	(20)

5	(ii) KIND (if peptide or protein):  (A) SEQUENCE ASSEMBLY METHOD: Overlap  (B) FRACMENT TYPE: Internal Fragment  (C) HYPOTHETICAL:  (iii) ORIGINAL SOURCE: HIV  (E) INDIVIDUAL ISOLATE:  (iv) IMMEDIATE SOURCE:  (C) CLONE:  (v) POSITION IN GENOME: Within Env Gene  (vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant  (viii) SEQUENCE DESCRIPTION:
15	SEQ ID NO: EE308-2
	1 5 10 15
	Cys Thr Arg Pro Asn Asn Thr Arg Lys Ser Ile His Ile Gly
20	TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA
	20 25 30
	Pro Gly Arg Pro Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asp Ile
25	CCA GGC AGA CCA TTT TAT ACA ACA GGA GAA ATA ATA GGA GAT ATA
	35
30	Arg Gln Ala His Cys AGA CAA GCA CAT TGT
35	(2) INFORMATION FOR SEQ ID NO: EE310-1 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 (B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single (D) TOPOLOGY: Linear
40	(D) TOPOLOGY: Linear  (ii) KIND: cDNA to genomic RNA  (ii) KIND (if peptide or protein):  (A) SEQUENCE ASSEMBLY METHOD: Overlap  (B) FRAGMENT TYPE: Internal Fragment
<b>45</b>	(C) HYPOTHETICAL:  (iii) ORIGINAL SOURCE: HIV  (E) INDIVIDUAL ISOLATE:  (iv) IMMEDIATE SOURCE:  (C) CLONE:  (v) POSITION IN GENOME: Within Env Gene
50	(vi) PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
	(viii) SEQUENCE DESCRIPTION:

SEQ ID NO: EE310-1 10 Cys Thr Arg Pro Ser Asn Asn Thr Arg Arg Gly Ile His Ile Gly TGT ACA AGA CCC AGC AAC AAT ACC AGA AGA GGT ATA CAT ATA GGA 30 20 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Thr Gly Asp Ile 10 CCA GGG AGA GCA TIT TAT ACA ACA GGA GAA ATA ACA GGA GAT ATA 35 15 Arg Gln Ala His Cys AGA CAA GCA CAT TGT INFORMATION FOR SEQ ID NO: EE310-2 (2) 20 SEQUENCE CHARACTERISTICS: (i) LENGTH: 105 (A) TYPE: Nucleic Acid (B) STRANDEDNESS: Single (C) TOPOLOGY: Linear (D) (ii) KIND: cDNA to genomic RNA (ii) KIND (if peptide or protein): SEQUENCE ASSEMBLY METHOD: Overlap (A) FRAGMENT TYPE: Internal Fragment (B) HYPOTHETICAL: (C) ORIGINAL SOURCE: HIV (iii) INDIVIDUAL ISOLATE: (iv) IMMEDIATE SOURCE: CLONE: POSITION IN GENOME: Within Env Gene (v) PROPERTIES OF SEQUENCE: Expresses conserved antigenic (vi) determinant SEQUENCE DESCRIPTION: (viii) SEQ ID NO: EE310-2

1 5 10 15

Cys Thr Arg Pro Ser Asn Asn Thr Arg Arg Gly Ile His Ile Gly

TGT ACA AGA CCC AGC AAC AAT ACA AGA AGA GGT ATA CAT ATA GGA

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20 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Thr Gly Asp Ile CCA GGG AGA GCA TIT TAT ACA ACA GGA GAA ATA ACA GGA GAT ATA 5 35 Arg Gln Ala His Cys AGA CAA GCA CAT TGT 10 INFORMATION FOR SEQ ID NO: EE310-3 (2) SEQUENCE CHARACTERISTICS: (i) LENGTH: 105 (A) TYPE: Nucleic Acid (B) STRANDEDNESS: Single 15 (C) TOPOLOGY: Linear (D) KIND: cDNA to genomic RNA (ii) KIND (if peptide or protein): (ii) SEQUENCE ASSEMBLY METHOD: Overlap (A) FRACMENT TYPE: Internal Fragment 20 (B) HYPOTHETICAL: (C) ORIGINAL SOURCE: HIV (iii) INDIVIDUAL ISOLATE: (E) IMMEDIATE SOURCE: (iv) 25 CLONE: (C) POSITION IN GENOME: Within Env Gene (v) PROPERTIES OF SEQUENCE: Expresses conserved antigenic (vi) determinant SEQUENCE DESCRIPTION: (viii) 30 SEQ ID NO: EE310-3 35 10 1 Cys Thr Arg Pro Ser Asn Asn Thr Arg Lys Gly Ile His Ile Gly TGT ACA AGA CCC AGC AAC AAT ACA AGA AAA GGT ATA CAT ATA GGA 25 40 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Thr Gly Asp Ile CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ACA GGA GAT ATA 45 35 Arg Gln Ala His Cys AGA CAA GCA CAT TGT

	(2)		INFO	RMAT	ION	FOR	SEQ	ID N	0: E	E311	-1					
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					(B)			: N			cid					
5					(C)			NDED			ingl	е				
					(D)			LOGY								
			(ii)	ı	KIND	: cD	NA t	o ge	nomi	c RN	Α					
			(ii)		KIND	(if	pep	tide	or	prot	ein)	:		_		
			•		(A)		SEQU	ENCE	ASS	EMBL	Y ME	THOD	): 0	verl	ap	
10					(B)		FRAC	MEN 1	TYP	E:	Inte	rnal	. Fra	gmen	t	
					(C)		HYPO	THE 1	'ICAL	: _						
			(iii	.)	ORIG	INAL	SOL	IRCE:	HIV	,						
			•	-	(E)		IND	VIDU	IAL I	SOLA	TE:					
			(iv)	)	IMME	TAIG	E SC	URCE	<b>:</b> :							
15					(C)		CLO	Æ:						-		
			(v)		POS1	TION	IN	GEN	ME:	With	nin E	inv (	Gene			
			(vi)	)				)F SI	QUEN	CE:	Ext	rese	ses c	conse	erved	antigenic
						ermic										
			(vii	ii)	SEQU	JENCE	E DES	SCRII	OIT?	i:						
20																
	SEQ	ID 1	<b>*0:</b>	EE3	11-1											
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25	1			_	. 5		<b>A</b>	787b	A		50-	TIA	Hic	Tio		
	Cys	Thr	Arg	Pro	Asn	ASD	AST	IRE	ACA	WLR	VCL	ATA	His	ATA	GGA	
	TGT	ACA	AGA	CCC	AAC	AAC	WAT	ACC	AGA	AUA	MOI	nin	CAT	*****	-	
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	Pro	GLY	Arg	ALS	rne	TAT	UCA WIS	ACA	CCA	CCT	ATA	ATA	GGA	GAT	ATA	
	CCA	GGG	AGA	GUA	111	TWI	Gun	nun	GGA	<b>301</b>						
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00	<b>A</b>	A	A1.	Т												
	Arg	Arg	WIR	TAT	Cys TGT											
	AGA	CGM	GLA	TUI	101											
40	(2)		TNE		TION	FOR	SEO	ID	NO:	EE31	2-1					•
	(2)		(i)		SEO	UENC	E CH	ARAC	TERI	STIC	s:				•	
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		(ii)	KIND (if peptide or protein): (A) SEQUENCE ASSEMBLY METHOD: Overlap (B) FRACMENT TYPE: Internal Fragment
5		(iii)	(C) HYPOTHETICAL: ORIGINAL SOURCE: HIV (E) INDIVIDUAL ISOLATE:
		(iv)	IMMEDIATE SOURCE: (C) CLONE:
10		(v)	POSITION IN GENOME: Within Env Gene PROPERTIES OF SEQUENCE: Expresses conserved antigenic
		(vi)	determinant
		(viii)	The second secon
15	SEQ ID	NO: EE3	12–1
			5 10 15
00	1 Cvs Thr	Arg Pro	Asn Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly
20	TGT ACA	AGG CCC	AAC AAC AAT ACA AGA AAA AGT ATA ACT ATA GGA
			20 25 30
25	Pro Glu	Arg Ala	Phe Tyr Ala Thr Asp Ile Ile Gly Asn Ile Arg
	CCA GAG	G AGA GCA	TIT TAT GCA ACA GAT ATA ATA GGA AAT ATA AGA
		#! - O	35
30	CAA GCA	A His Cys	
	<b>U</b>	-	
	(2)	TNFORM	ATION FOR SEQ ID NO: EE312-2
<b></b>	(2)	(i)	SEQUENCE CHARACTERISTICS:
35			(A) LENGTH: 99 (B) TYPE: Nucleic Acid
			(B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single
			(D) TOPOLOGY: Linear
40		(ii)	KIND: cDNA to genomic RNA KIND (if peptide or protein):
		(ii)	(A) SEQUENCE ASSEMBLY METHOD: Overlap
			(B) FRACMENT TYPE: Internal Fragment
		(111)	(C) HYPOTHETICAL:ORIGINAL SOURCE: HIV
45		(iii)	(E) INDIVIDUAL ISOLATE:
		(iv)	IMMEDIATE SOURCE:
		()	(C) CLONE:
	•	(v) (vi)	PROPERTIES OF SEQUENCE: Expresses conserved antigenic
50		(/	determinant
		(viii)	SEQUENCE DESCRIPTION:

SEQ ID NO: EEE312-2 10 1 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly 5 TGT ACA AGG CCC AAC AAC AAT ACA AGA AAA AGT ATA ACT ATA GGA 20 Pro Gly Arg Ala Phe Tyr Ala Thr Asp Ile Ile Gly Asn Ile Arg 10 CCA GGG AGA GCA TTT TAT GCA ACA GAT ATA ATA GGA AAT ATA AGA 35 15 Gln Ala His CAA GCA CAT INFORMATION FOR SEQ ID NO: EE313-1 (2) 20 SEQUENCE CHARACTERISTICS: (i) LENGTH: 105 (A) TYPE: Nucleic Acid (B) STRANDEDNESS: Single (C) TOPOLOGY: Linear (D) 25 KIND: cDNA to genomic RNA (ii) KIND (if peptide or protein): (ii) SEQUENCE ASSEMBLY METHOD: Overlap (A) -FRAGMENT TYPE: Internal Fragment (B) HYPOTHETICAL: (C) 30 ORIGINAL SOURCE: HIV (iii) INDIVIDUAL ISOLATE: (E) IMMEDIATE SOURCE: (iv) CLONE: (C) POSITION IN GENOME: Within Env Gene (v) PROPERTIES OF SEQUENCE: Expresses conserved antigenic 35 (vi) determinant SEQUENCE DESCRIPTION: (viii) 40 SEQ ID NO: EE313-1

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Cys Thr Arg Pro Asn Asn His Thr Glu Lys Arg Ile Thr Leu Gly TGT ACA AGA CCC AAC AAC CAT ACA GAA AAA CGT ATA ACT CTA GGA

					20					25				•	30		
	Pro	G1v	Arg	Va1	Leu	Tyr	Thr	Thr	G1y	Arg	Ile	Ile	G1y	Asp	Ile		
	CCG	GGG	AGA	GTA	CTT	TAT	ACA	ACA	GGA	AGA	ATA	ATA	GGA	GAT	ATA		
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	Aro	Arg	Ala	His	Cvs												
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	(2)		TNF	)RMA'	CION	FOR	SEO	ID I	10: E	E317	7–1						
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	CEO	TD 1	NO.	EE3	171						• •					•	
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		The sec	A	Dro		Aen	Acn	Thr	Ara		Ser	Tle	Thr	Ile	Gly		
	TOT	TIII	VCV	CCC	AAT	AAC	AAT	ACA	AGA	AAA	AGT	ATA	ACT	ATA	GGA		
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	Pro	GIY	Arg	ATS	TTT	TAT	WIR	YCV	CCA	GAA	ΔΤΔ	ልሞል	CCA	CAT	ATA		
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	AGA	CAA	GCA	CAT	TGT												
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	(2)		INFO	)RMA]	CION											
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15			(iv)	)		CAIG		OURCI	3:							
					(C)		CLO							-		
			(v)		POSI	TION	IN	GEN	ME:	With	nin l	nv (	ene			
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20			(vi	ii)	SEQU	JENCE	S DES	SCRII	PTIO	<b>v:</b>						
	SEQ	ID 1	10:	EE3	20–1											
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25	1		•		5					10					15	
		The	A=0	Pro	Asn	Aen	Agn	Thr	Aro		Ser	Ile	His	I1e		
	TOT	ACA	VCV	CCC	AAC	AAC	AAT	ACA	AGA	AAA	AGT	ATA	CAT	ATA	GGA	
	101	non	11011	000	1110	1410										
- 30																
					20					25					30	
	Pro	G1v	Arg	Ala	Phe	Tyr	Ala	Thr	G1y	G1u	Ile	Ile	G1y	Asp	Ile	
	CCA	GGG	AGA	GCA	TTT	TAT	GCA	ACA	GGA	GAA	ATA	ATA	GGA	GAT	ATA	
35			•													
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	Arg	G1n	Ala	His	Cys											
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5			(iii		(E)		IND	[VIDI	JAL 1		ATE:				<u></u> .		
			(iv)		(C)	EDIAT	CLO	E:				· 		_			
10			(v) (vi)		PROI	TION PERTI	ES (							cons	erved	antig	enic
			(vi	li)		JENCI		SCR II	PTION	l:							
15	SEQ	ID P	10:	EE32	20–2												
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2Ò	Сув	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile	His	Ile	G1y		
	TGT	ACA	AGA	CCC	AAC	AAC	AAT	AUA	AGA	AAA	AGI	AIA	CAT	WIW	GGA		
					20					25					30		
25	Pro	G1y	Arg	Ala	Phe	Tyr	Thr	Thr	Gly	Glu	Ile	Ile	G1y	Asp	Ile		
25	CCA	GGC	AGA	GCA	TTT	TAT	ACA	ACA	GGA	GAA	ATA	ATA	GGA	GAT	ATA		
					35												
30			Ala														
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35			(i)			UENC					S:						
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50			(vi	)					EQUE	NCE:	Ex	pres	ses	cons	erved	antig	enic
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SEQ ID NO: EE322-1 10 5 5 1 Thr Arg Pro Gly Asn Asn Thr Arg Lys Gly Ile His Ile Gly Pro ACA AGA CCC GGC AAC AAT ACA AGA AAA GGT ATA CAT ATA GGA CCA 10 25 20 Gly Arg Ala Ile Tyr Ala Thr Asp Ile Ile Gly Asp Ile Arg Gln CGC AGA GCA ATT TAT GCA ACA GAT ATA ATA GGA GAT ATA AGA CAA 15 35 Ala His Cys GCA CAT TGT INFORMATION FOR SEQ ID NO: EE322-2 20 (2) SEQUENCE CHARACTERISTICS: (i) LENGTH: 105 (A) TYPE: Nucleic Acid (B) STRANDEDNESS: Single (C) TOPOLOGY: Linear 25 (D) KIND: cDNA to genomic RNA (ii) KIND (if peptide or protein): (ii) SEQUENCE ASSEMBLY METHOD: Overlap (A) FRAGMENT TYPE: Internal Fragment (B) 30 (C) HYPOTHETICAL: ORIGINAL SOURCE: HIV (iii) INDIVIDUAL ISOLATE: (E) IMMEDIATE SOURCE: (iv) CLONE: (v) POSITION IN GENOME: Within Env Gene 35 PROPERTIES OF SEQUENCE: Expresses conserved antigenic (vi) determinant SEQUENCE DESCRIPTION: (viii) 40 SEQ ID NO: EE322-2 5 10

93

Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Pro Ile Gly

TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CCT ATA GGA

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					20					25					30		
	Pro	G1y	Arg	Ala	Phe	Tyr	Thr	Thr	G1y	Glu	Ile	Ile	G1y	Asp	Ile		
	CCA	GGG	AGA	GCA	TTT	TAT	ACA	ACA	GGA	GAA	ATA	ATA	GGA	GAT	ATA		
5																	
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	<b>A</b> .	<b>61</b> .	41-	** 1 -	35												
			Ala GCA														
	AGA	CAA	GUA	CWI	161												
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20					(B)			GMEN.									
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	,		(ii:	i)	ORI	GINA	L SO	URCE	: HIV	J							
					(E)		IND	IVID	JAL :	ISOL	ATE:						
25			(iv	)				OURC	E:								
					(C)		CLO			111 A	-4- 1	P (	2	-			
			(v)					GEN							arvad	antigeni	_
			(vi	,		ermi:		OF SI	eQue.	VCE.	III.	bres	BCD '	COMS	erveu	. antigeni	٠
	•		(vi	ii)		-		SCRI	PTIO	N:					•		
30			<b>\'</b>	,													
	SEQ	ID I	NO:	EE3	22–3												
35					5					10					15		
	1 0	Th-	A =~	Dro		Aen	Acn	Thr	Δτσ		Ser	Tle	Thr	Tle			
	TOT	TUE	VCV	CCC	TAA	AAC	AAT	ACA	AGA	AAA	AGT	ATA	ACT	ATA	GGA		
	191	11011	21011	000		1210					-20-						
40	,				20				•	25					30		
								Thr									
	CCA	GGG	AGA	GCA	TIT	TAT	GCA	ACA	GGA	GAA	ATA	ATA	GGA	GAT	ATA		
				•													
45					35												
	Ara	G1n	Ala	Hic													
			GCA														
		~~ a. 1															
50																	

	(2)	INFORMA	TION FOR SEQ ID NO: EE324-1
	` '	(i)	SEQUENCE CHARACTERISTICS:
			(A) LENGTH: 105
_			(B) TYPE: Nucleic Acid
5			(C) STRANDEDNESS: Single
			(D) TOPOLOGY: Linear
		(ii)	KIND: cDNA to genomic RNA
		(ii)	KIND (if peptide or protein):
			(A) SEQUENCE ASSEMBLY METHOD: Overlap
10			(B) FRACMENT TYPE: Internal Fragment
			(C) HYPOTHETICAL:
		(iii)	ORIGINAL SOURCE: HIV
			(E) INDIVIDUAL ISOLATE:
		(iv)	IMMEDIATE SOURCE:
15			(C) CLONE:
		(v)	POSITION IN GENOME: Within Env Gene
		(vi)	PROPERTIES OF SEQUENCE: Expresses conserved antigenic
		• •	determinant
		(viii)	SEQUENCE DESCRIPTION:
20			
	SEQ ID	NO: EE3	24–1
25	1		5 10 15
		Arg Pro	Asn Asn Asn Thr Ile Lys Ser Ile His MET Gly
	TGT ACA	AGA CCC	AAC AAC AAT ACA ATA AAA AGT ATA CAT ATG GGA
			•
30			20 25 30
	Leu Gly	Arg Thr	Phe Tyr Thr Thr Gly Glu Val Ile Gly Asp Ile
	CTA GGG	AGG ACA	TTT TAT ACA ACA GGA GAA GTA ATA GGA GAT ATA
35			
55			35
		n Ala His	
	AGA CAA	GCA CAT	TGT
40	(0)	TAIDODAA	TION FOR SEC ID NO. FE391-9
	(2)		TION FOR SEQ ID NO: EE324-2
		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 105
45			
		(11)	(D) TOPOLOGY: Linear KIND: cDNA to genomic RNA
		(ii)	VIND. COMP CO REHOMIC WAY

5			(ii)	)	KINI (A) (B) (C)	) (if	SEQU FRAC	JENCE MENT	or E ASS T TYI	EMBI E:	Y MI	): ETHOI ernal			_		
3			(iii	L)		INAI	SOU	IRCE:	HIV	,	TE:						
			(iv)		(C)	CAIG	CLO	Œ:		*****				-			
10			(v) (vi)		PROP		ES (					eress		conse	erved	antigeni	c
			(vii	ii)				SCRII	PTIO	V:							
15	SEQ	ID 1	10:	EE32	24–2			,									
	1				5					10					15		
20	Cvs	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile	His	Leu	Gly		
	TGT	ACA	AGA	CCC	AAC	AAC	AAT	ACA	AGA	AAA	AGT	ATA	CAT	CTA	GGG		
					20					25					30		
25	Pro	G1y	Arg	Ala	Phe	Tyr	Thr	Thr	Gly	qaA	Ile	Ile	Gly	Asp	Ile		
	CCA	GGG	AGA	GUA	TIT	TAI	AUA	AUA	GGA	GAU	WIW	ATA	GGA	GAI	VIV		
					35												
30			Ala GCA														
	GGA	UAA	GCA	wi	161				-								
	<i>(</i> - )		****		<b>***</b>	EOD.	020	TD :	MO	BB30'	7 1						
	(2)		(i)	UKMA					NO: : TERI:								
35			(1)		(A)			GTH:									
					(B)		TYP	<b>E:</b> 1	Nuc1	eic A	Acid						
					(C)				DNES		Sing	1e					
			<i>(</i> : :		(D)	D		OLOG		Line							
40			(ii (ii						enom e or			):					
			(11	,	(A)	<b>-</b> (-						ETHO	D:	0ver	lap		
					(B)				T TY		Int	erna	l Fr	agme	nt		
				_	(C)				TICA								
45			(ii	i)					: HI		4 TP 4						
			(iv	`	(E)	EDIA			UAL E:	1901	WID:					<del></del>	
			(TA	,	(C)		CTO										
			(v)		POS	ITIO	N IN	GEN				Env					
ĖO			(vi	)					EQUE	NCE:	Ex	pres	ses	cons	erved	antigeni	ic
50			, .			ermi			nera	<b>31</b> -							
			(vi	ii)	SEQ	ORNC	E DE	<b>SUKI</b>	PTIO	u:							

SEQ ID NO: EE327-1

5 1 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His Ile Gly 5 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA GGT ATA CAT ATA GGA 25 20 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile 10 CCA GGG AGA GCA TTT TAT GCA ACA GGA GAC ATA ATA GGA GAT ATA 35 15 Arg Gln Ala His Cys AGA CAA GCA CAT TGT INFORMATION FOR SEQ ID NO: EE327-2 (2) 20 (i) SEQUENCE CHARACTERISTICS: LENGTH: 105 (A) TYPE: Nucleic Acid (B) STRANDEDNESS: Single (C) TOPOLOGY: Linear (D) KIND: cDNA to genomic RNA 25 (ii) KIND (if peptide or protein): (ii) SEQUENCE ASSEMBLY METHOD: Overlap (A) FRACMENT TYPE: Internal Fragment (B) (C) HYPOTHETICAL: ORIGINAL SOURCE: HIV 30 (iii) INDIVIDUAL ISOLATE: (E) IMMEDIATE SOURCE: (iv) CLONE: (C) POSITION IN GENOME: Within Env Gene (v) PROPERTIES OF SEQUENCE: Expresses conserved antigenic 35 (vi) determinant SEQUENCE DESCRIPTION: (viii) 40 SEQ ID NO: EE327-2 10 1 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His Ile Gly

TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA GGT ATA CAT ATA GGA

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					20					25					30		
	_	o1	<b>A</b>	A1.	20 Phe	Ture .	۱a '	Thr (	31 <b>v</b> A	sp 1	le:	Ile (	31y <i>f</i>	lsp	Ile		
	Pro	CCC	ACA	UCV HIM	TTT :	PAT :	GCA	ACA (	GGA (	AC A	TA A	ATA (	GGA (	AT .	ATA		
	CCA	GGG	MGM	GUA	111 .												
5																	
					35												
	Arg	Gln	Ala	His	Tyr												
	AGA	CAA	GCA	CAT	TAT												
10							050	TD N	A - 171	F297.	_3						
	(2)			)RMA1	ION SEQU	FUK PMOE	DEQ DEQ	DACT TU M	PD TC'	TTCS	•						
			(i)		(A)	ENCE	TENC	TH:	105	1100	•						
					(B)		TYPE	: N		ic A	cid						
15					(C)			NDED			ingl	e					
					(D)			LOGY		inea	r						
			(ii	)	KIND	: cI	NA t	o ge	nomi	c RN	A						
			(ii		KIND	(if	net	stide	or	prot	ein)	:	_	٠.			
			•-	•	(A)		SEQU	ENCE	ASS	embl	Y ME	THOL	:_ 0	verl	Lap		
20					(B)			MENT			Inte	rnal	Fra	gmer	זכ		
					(C)			THE									
			(ii	i)		INAJ	S01	JRCE:	HIV	COT A	TIP .						
					(E)			IV IDI		DULM	110+						
25			(iv	)	(C)	DIA.	CLO	DURCI	•					_			
			(\		DOC 1	TIO	u TN	GEN	ME:	With	in l	inv (	ene	_			
			(v)		DOC 1	TIO	u TN	GEN	ME:	With	in l	inv (	ene ses c	cons	erved	anti	genic
			(v) iv)		POS1	ERT	N IN IES	GENO OF SI	ME: EQUEN	With ICE:	in l Ex	inv (	Gene Ges (	cons	erved	anti	genic
			(vi	)	POSI PROI dete	ERT rmi	N IN IES nant	GEN OF SI	EQUEN	ice:	in l Ex	inv (	ene ses (	cons	erved	anti	genic
30	·		(vi		POSI PROI dete	ERT rmi	N IN IES nant	GENO OF SI	EQUEN	ice:	in l Ex	inv (	Sene Ses (	cons	erved	anti	genic
30	·		(vi	) ii)	POSI PROI dete SEQU	ERT rmi	N IN IES nant	GEN OF SI	EQUEN	ice:	in l Ex	inv (	Sene ses (	cons	erved	anti	genic
30	SEQ	ID	(vi	) ii)	POSI PROI dete	ERT rmi	N IN IES nant	GEN OF SI	EQUEN	ice:	in l Ex	Env (	Sene ses (	cons	erved	anti	genic
30	SEQ	ID	(vi	) ii)	POSI PROI dete SEQU	ERT rmi	N IN IES nant	GEN OF SI	EQUEN	ice:	in l	Env ( press	Gene ses (	cons	erved	anti	genic
	_	ID	(vi	) ii)	POSI PROI dete SEQU	ERT rmi	N IN IES nant	GEN OF SI	EQUEN	ice:	in l	Env ( press	Gene ses (	conse	erved	anti	genic
30 35	1		(vi (vi NO:	ii) EE3	POSI PROI dete SEQU 27-3	PERT PERT PENC	N IN IES mant E DE	GENCOF SI	PTION	ICE: V: 10	Ex	ile	His	Ile	15 Gly	anti	genic
	1		(vi (vi NO:	ii) EE3	POSI PROI dete SEQU 27-3	PERT PERT PENC	N IN IES mant E DE	GENCOF SI	PTION	ICE: V: 10	Ex	ile	His	Ile	15 Gly	anti	genic
	1		(vi (vi NO:	ii) EE3	POSI PROI dete SEQU 27-3	PERT PERT PENC	N IN IES mant E DE	GENCOF SI	PTION	ICE: V: 10	Ex	ile	His	Ile	15	antiį	genic
	1		(vi (vi NO:	ii) EE3	POSI PROI dete SEQU 27-3	PERT PERT PENC	N IN IES mant E DE	GENCOF SI	PTION	ICE: V: 10	Ex	ile	His	Ile	15 Gly GGA	anti	genic
	1 Cys TGT	Th:	(vi (vi NO:	ii) EE3	POSI PROI dete SEQU 27-3	PERT PERT PENC PENC Asn AAC	Asn	GENO OF SI SCRII	PTION PTION Arg AGA	ICE: I: 10 Lys AAA	Gly GGT	Ile ATA	His CAT	Ile ATA	15 G1y GGA	anti	genic
35	1 Cys TGT	The AC	(vi (vi NO:	ii) EE3 Pro	POSI PROI dete SEQU 27-3 5 Asn AAC	Asn AAC	N IN IES nant E DE	GENGOF SI SCRII	Arg AGA	ICE: I: 10 Lys AAA 25 Asp	Gly	Ile ATA	His CAT	Ile ATA	15 Gly GGA 30 o Ile	anti	genic
35	1 Cys TGT	The AC	(vi (vi NO:	ii) EE3 Pro	POSI PROI dete SEQU 27-3 5 Asn AAC	Asn AAC	N IN IES nant E DE	GENGOF SI SCRII	Arg AGA	ICE: I: 10 Lys AAA 25 Asp	Gly	Ile ATA	His CAT	Ile ATA	15 Gly GGA	anti	genic
35	1 Cys TGT	The AC	(vi (vi NO:	ii) EE3 Pro	POSI PROI dete SEQU 27-3 5 Asn AAC	Asn AAC	N IN IES nant E DE	GENGOF SI SCRII	Arg AGA	ICE: I: 10 Lys AAA 25 Asp	Gly	Ile ATA	His CAT	Ile ATA	15 Gly GGA 30 o Ile	anti	genic
35 40	1 Cys TGT	The AC	(vi (vi NO:	ii) EE3 Pro	POSI PROI dete SEQU 27-3 5 Asn AAC	Asn AAC	N IN IES nant E DE	GENGOF SI SCRII	Arg AGA	ICE: I: 10 Lys AAA 25 Asp	Gly	Ile ATA	His CAT	Ile ATA	15 Gly GGA 30 o Ile	anti	genic
35	1 Cys TGT Pro	The AC	(vi (vi NO: A AGA Y Arg	ii) EE3 Pro	POSI PROI dete SEQU 27-3 5 Asn AAC	Asn AAC	N IN IES nant E DE	GENGOF SI SCRII	Arg AGA	ICE: I: 10 Lys AAA 25 Asp	Gly	Ile ATA	His CAT	Ile ATA	15 Gly GGA 30 o Ile	anti	genic
35 40	1 Cys TGT Pro CCA	The AC	(vi (vi NO: A AGA Y Arg G AGA	ii) EE3 Prod CCC	POSI PROI dete SEQU 27-3 5 Asn AAC 20 Phe TTT	Asn AAC Tyr	N IN IES nant E DE	GENGOF SI SCRII	Arg AGA	ICE: I: 10 Lys AAA 25 Asp	Gly	Ile ATA	His CAT	Ile ATA	15 Gly GGA 30 o Ile	anti	genic
35 40	1 Cys TGT Pro CCA	The AC	(vi (vi NO: A AGA Y Arg G AGA	ii) EE3 Prod CCC	POSI PROI dete SEQU 27-3 5 Asn AAC	Asn AAC Tyr	N IN IES nant E DE	GENGOF SI SCRII	Arg AGA	ICE: I: 10 Lys AAA 25 Asp	Gly	Ile ATA	His CAT	Ile ATA	15 Gly GGA 30 o Ile	anti	genic

	(2)		INFO	RMAT	ION	FOR	SEQ	ID N	0: E	E345	-1						
	\-/		(i)		SEQU	ENCE	CHA	RACT	ERIS	TICS	:						
			• •		(A)		LENG		105								
					(B)					ic A	cid						
5					(c)		STRA	NDED	ness	: S	ingl	е					
					(D)		TOPO	LOGY	: I	inea	r						
			(ii)	)	KIND	: cD	NA t	o ge	nomi	c RN	Α						
			(ii)		KIND	(if	per	tide	or	prot	ein)	:					
			<b>\</b> ,		(A)		SEQU	ENCE	ASS	EMBL	Y ME	THOD	): 0	verl	ар		
10					(B)			MENT			Inte	rnal	Fra	gmen	t		
					(c)		HYPO	THE	'ICAI	.: _							
			(iii	<b>(</b> )	ORIG	INAL	SOU	RCE:	HIV	•							
			<b>\_</b>	•	(E)		IND	VIDU	IAL I	SOLA	TE:					<del></del>	
			(iv)	)	IMME	TAIC	E SC	URCE	<b>:</b> :								
15			(,		(c)		CLON	E:						_			
			(v)		POST	TION	IN	GEN	ME:	With	in E	inv (	ene				
			(vi)		PROP	ERTI	ES (	F SI	EQUE	ICE:	Exp	rese	es c	onse	rved	antigeni	C
				•	dete												
			(vii	ii)	SEQU	ENCE	DES	SCR 11	OIT?	<b>i</b> :							
20			•	-	•												
	SEQ	ID 1	10:	EE3	<b>45−1</b>												
	- •																
															15		
25	1				5					10	-1	<b>-1</b> -	W. 1 -	T1.			
	Cys	Thr	Arg	Pro	Ser	Asn	Asn	Thr	Arg	Lys	GIA	TTE	H18	116	CCC	•	
	TGT	ACA	AGA	CCC	AGC	AAT	AAT	ACA	AGA	AAA	GGT	ATA	CAT	AIA	GGG		
30										0.5					30		,
30					20	_		_	<b>~1</b> -	25	T1 -	77%	C1	Aan			
	Pro	Gly	Arg	Ala	Phe	Tyr	Ala	Thr	GIA	GIU	116	THE	GLA	CAT	ATA		
	CCA	GGG	AGA	GCA	TTT	TAT	GCA	AUG	GGA	GAG	ATA	ACA	GGA	GAI	HIA		
35				•													
33			_		35											•	
	Arg	G1n	Ala	His	Cys												
	AGA	CAA	GCA	CAT	TGT												
40									NO -	BB31.	<b>5</b> 2						
40	(2)				TION	FOR	SEQ	LD	NU:	BB34 CTTO	5-Z				•		
			(i)		_					STIC	5:						
					(A)			GTH:		-	A - 1 3						
					(B)		TYP			eic .							
45					(C)			ANDE		_	Sing	те					
45					(D)			OLOG		Line	_						
			(ii	.)	KIN	D: c	DNA	to g	enon	ic R	AM						

_		(ii)	KIND (if peptide or protein):  (A) SEQUENCE ASSEMBLY METHOD: Overlap  (B) FRAGMENT TYPE: Internal Fragment  (C) HYPOTHETICAL:
5		(iii)	ORIGINAL SOURCE: HIV (E) INDIVIDUAL ISOLATE:
		(iv)	IMMEDIATE SOURCE:  (C) CLONE:
10		(v)	POSITION IN GENOME: Within Env Gene PROPERTIES OF SEQUENCE: Expresses conserved antigenic
		(vi)	determinant
		(viii)	The same of the sa
		(4111)	DDQ DDQ DDQ DDQ DDQ
15	SEQ ID	NO: EE3	45–2
			5 10 15
	1 _		Ser Asn Asn Thr Arg Lys Gly Ile His Ile Gly
20	Cys Th	r Arg Pro	AGC AAT AAT ACA AGA AAA GGT ATA CAT ATA GGG
	IGI AG	n nun coc	
			25 30
25	Pro G1	y Arg Ala	Phe Phe Thr Thr Gly Glu Ile Thr Gly Asp Ile TTT TTT ACA ACA GGA GAA ATA ACA GGA GAT ATA
	CCA GG	G AGA GUA	. TIT III ACA ACA GGA GGA IIII IIII
			•
			35
30	Arg G1	n Ala His	Cys
	AGA CA	A GCA CAT	TGT
		•	
	(2)	INFORM	ATION FOR SEQ ID NO: EE345-3
oc.	, ,	(i)	SEQUENCE CHARACTERISTICS:
35			(A) LENGTH: 105
			(B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single
		(ii)	(D) TOPOLOGY: Linear KIND: cDNA to genomic RNA
40		(ii)	KTND (if peptide or protein):
		(/	(A) SEQUENCE ASSEMBLY METHOD: Overlap
			(B) FRACMENT TYPE: Internal Fragment
			(C) HYPOTHETICAL:
45		(iii)	ORIGINAL SOURCE: HIV
40			(E) INDIVIDUAL ISOLATE:
		(iv)	IMMEDIATE SOURCE: (C) CLONE:
		(v)	POSITION IN GENOME: Within Env Gene
		(vi)	ontigenic
50			determinant
		(viii)	SEQUENCE DESCRIPTION:

SEQ ID NO: EE345-3

10 Cys Thr Arg Pro Ser Asn Asn Thr Arg Lys Ser Ile His Ile Gly TGT ACA AGA CCC AGC AAT AAT ACA AGA AAA AGT ATA CAT ATA GGG 30 25 20 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Thr Gly Asp Ile 10 CCA GGG AGA GCA TIT TAT GCA ACG GGA GAG ATA ACA GGA GAT ATA 35 15 Arg Gln Ala His Cys AGA CAA GCA CAT TGT INFORMATION FOR SEQ ID NO: EE356-1 (2) SEQUENCE CHARACTERISTICS: 20 (i) LENGTH: 105 (A) TYPE: Nucleic Acid (B) STRANDEDNESS: Single (C) TOPOLOGY: Linear (D) KIND: cDNA to genomic RNA 25 (ii) KIND (if peptide or protein): (ii) SEQUENCE ASSEMBLY METHOD: Overlap (A) FRACMENT TYPE: Internal Fragment (B) HYPOTHETICAL: (C) ORIGINAL SOURCE: HIV 30 (iii) INDIVIDUAL ISOLATE: (E) IMMEDIATE SOURCE: (iv) (C) CLONE: POSITION IN GENOME: Within Env Gene (v) PROPERTIES OF SEQUENCE: Expresses conserved antigenic 35 (vi) determinant (viii) SEQUENCE DESCRIPTION: 40 SEQ ID NO: EE356-1 5 10 1 Cys Ile Arg Pro Ser Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly TGT ATA AGA CCC AGC AAC AAT ACA AGA AAA AGT ATA ACT ATA GGA 45

55

	Pro Gly	Arg Ala AGA GCA	20 25 30 Phe Phe Ala Thr Gly Glu Ile Thr Gly Asp Ile TIT TIT GCA ACA GGA GAA ATA ACA GGA GAT ATA	
5	Arg Gln AGA CAA	Ala His GCA CAT	35 Cys TGT	
10				
	(2)	INFORMAT	TION FOR SEQ ID NO: EE356-2 SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 (B) TYPE: Nucleic Acid	
15			(C) STRANDEDNESS: Single (D) TOPOLOGY: Linear	
		(ii) (ii)	KIND: cDNA to genomic RNA KIND (if peptide or protein): (A) SEQUENCE ASSEMBLY METHOD: Overlap	
20		(iii)	(B) FRAGMENT TYPE: Internal Fragment (C) HYPOTHETICAL: ORIGINAL SOURCE: HIV	
25		(iv)	(E) INDIVIDUAL ISOLATE: IMMEDIATE SOURCE: (C) CLONE:	
		(v) (vi)	POSITION IN GENOME: Within Env Gene PROPERTIES OF SEQUENCE: Expresses conserved antigen determinant	ic
			GC CCAMALICATO	
30		(viii)	SEQUENCE DESCRIPTION:	
30	SEQ ID		SEQUENCE DESCRIPTION: 356-2	
30 35	1	NO: EE3	356–2 5 10 15	
	1 Cwc 11e	NO: EE3	356–2	
<b>35</b>	1 Cwc 11e	NO: EE3	356-2  5 10 15  5 Ser Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly C AGC AAC AAT ACA AGA AAA AGT ATA ACT ATA GGA	
	1 Cys Ile TGT ATA	Arg Pro	356-2  5 10 15  5 Ser Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly C AGC AAC AAT ACA AGA AAA AGT ATA ACT ATA GGA	
<b>35</b>	1 Cys Ile TGT ATA	Arg Pro	356-2  5 10 15  5 Ser Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly C AGC AAC AAT ACA AGA AAA AGT ATA ACT ATA GGA	
<b>35</b>	1 Cys Ile TGT ATA	Arg Pro	356-2  5 10 15 0 Ser Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly C AGC AAC AAT ACA AGA AAA AGT ATA ACT ATA GGA  20 25 30 a Phe Phe Ala Thr Gly Glu Ile Thr Gly Asp Ile	
35	1 Cys Ile TGT ATA Pro Gly CCA GGG	Arg Pro	356-2  5 10 15 0 Ser Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly C AGC AAC AAT ACA AGA AAA AGT ATA ACT ATA GGA  20 25 30 a Phe Phe Ala Thr Gly Glu Ile Thr Gly Asp Ile A TTT TTT GCA ACA GGA GAA ATA ACA GGA GAT ATA  35 s Cys	

	(2)			RMAT	ION	FOR	SEQ	ID N	0: E	E356	-3					
			(i)		SEQU						•					
					(A)		LENG	: N	105		.i.a					
5					(B)						ingl	_				
3					(C)			NDED			_					
					(D) KIND										•	
			(ii)		KIND	11 CL	MA L	o ge	HOMI	nrot	ein)	•				
			(ii)	ı	(V)	(11	SEUL	ENCE	ASS	EMRI	Y MF	THOL	): O	verl	.ap	
10					(B)			MENT			Inte	rnal	Fre	emen	ıt	
					(C)			THE								
			(iii	``				RCE:								
			(111	- /	(E)			VIDU			TE:					
			(iv)	)		CATC		URCE								
15			(14)	,	(C)		CLO	IE:						-		
			(v)		POST	TION	ITN	GENO	ME:	With	in E	nv (	Sene			
			(vi)	)	PROP	ERT	ES C	)F SE	QUE	ICE:	Exp	pres	ses (	conse	erved	antigenic
					dete											
			(vii	ii)	SEQU	JENCI	E DES	SCRII	PTIOI	i:						
20																
	SEO	TD 1	10:	EE35	56-3											
	524															
25	•				5					10					15	
	1	T1_	A	Pro	502	Aon	Aen	Thr	Aro		Ser	Ile	Thr	Ile	G1y	
	TOT	116	VCV	CCC	ACC	AAC	AAT	ACA	AGA	AAA	AGT	ATA	ACT	ATA	GGA	
	161	WIW	AUA	CCC	AGO	1210			•							
															•	
30					20					25					30	
	Pro	G1v	Arg	Ala	Phe	Phe	Ala	Thr	G1y	Glu	Ile	Thr	G1y	Asp	Ile	
	CCA	GGG	AGA	GCA	TTT	TTT	GCA	ACA	GGA	GAA	ATA	ACA	GGA	GAT	ATA	
35					35											
	_			His												
	AGA	CAA	GCA	CAT	TGT											
40	(2)		TME	ORMA'	TTON	<b>P</b> OD	SRO	TD	NO:	RE35	9–1					
	(2)		(i)		CEU	TURNO	R CH	ARAC	TER I	STIC	s:				•	
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			(iii	L )	(E)	TWAT			JAL J		TE:						
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15	SEQ	ID 1	40:	EE35	9–1												
	1				5					10					15		
20	Cvs	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Arg	Ser	Ile	Asn	Ile	G1y		
20	TGT	ACA	AGA	CCC	AAC	AAC	AAT	ACA	AGA	AGA	AGT	ATA	AAT	ATA	GGA		
					20					25					30		
25	Pro	G1y	Arg	Ala	Phe	Tyr	Ala	Thr	G1y	Asp	Ile	Ile	G1y	Asp	Ile		
	CCA	GGG	AGA	GCC	TTT	TAT	GCA	ACA	GGA	GAC	ATA	ATA	GGA	GAT	ATA		
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30			Ala														•
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			(v)		POS	ITIO	N IN	GEN	OME:	Wit	hin	Env	Gene				
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SEQ ID NO: EE359-2

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5	1 Cys Thr Arg P TGT ACA AGA C	5 10 15 TO Asn Asp Asn Thr Arg Arg Ser Ile Asn Ile Gly CC AAC GAC AAT ACA AGA AGA AGT ATA AAT ATA GGA
10	Pro Gly Arg A CCA GGG AGA G	20 25 30 La Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile CC TTT TAT GCA ACA GGA GAC ATA ATA GGA GAT ATA
15	Arg Gln Ala H AGA CAA GCA C	
20	(2) INFOR	MATION FOR SEQ ID NO: EE359-3 SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 (B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single
<b>25</b>	(ii) (ii)	(D) TOPOLOGY: Linear KIND: cDNA to genomic RNA KIND (if peptide or protein): (A) SEQUENCE ASSEMBLY METHOD: Overlap (B) FRAGMENT TYPE: Internal Fragment
30	(iii)	(E) INDIVIDUAL ISOLATE: IMMEDIATE SOURCE: (C) CLONE:
35	(v) (vi) (viii	determinant
40	SEQ ID NO: I	E359–3 .
45	1 Cys Thr Arg I TGT ACA AGA (	5 10 15 TO ASD ASD ASD Thr Arg Arg Ser Ile ASD Ile Gly CC AAC GAC AAT ACA AGA AGA AGT ATA AAT ATA GGA

					20					25					30	
	Pro	Gly	Arg	Ala	Phe	Tyr	Ala	Thr	Gly	Asp	Ile	Ile	Gly	Asp	Ile	
	CCA	GGG	AGA	GCC	TTT	TAT	GCA	ACA	GGA	GAC	ATA	ATA	GGA	GAT	ATA	
_																
5																
					35											
	Arg	G1n	Ala	His	Cvs											
				CAT												
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	(2)		INF	ORMA'	rion	FOR	SEQ	ID I	10: 1	<b>E36</b> 0	0-1					
	ν-,		(i)					ARAC'								
			<b>\</b> _,		(A)			GTH:	105	_						
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15					(c)		STR	ANDEI	)NES	s: s	Sing	le				
					(D)		TOP	OLOG	<b>7:</b> 1	Linea	ar					
			(ii	)		): cl		to ge		ic Ri	NA.					
			(ii					ptide				):				
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20					(B)		-	GMEN.						agmer		
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			(vi												erved	antigenic
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35	1				5					10					15	
	Cys	Thr	Arg	Pro	Ser	Asn	Asn	Thr	Arg	Lys	Ser	Ile	His	Ile	Ala	
,	TGC	ACA	AGG	CCC	AGC	AAC	AAT	ACA	AGA	AAA	AGT	ATA	CAT	ATA	GCA	
40					20					25					30	
	Pro	G1y	Arg	Ala	Phe	Tyr	Thr	Thr	G1y	Ala	Ile	Thr	G1y	Asp	Ile	
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45					35											
	Arg	Gln	Ala	His	Cys											
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	(2)			ORMA'	CION	FOR	SEQ	ID I	10: E	E360	)-2						
			(i)			ENCE			TER IS		3:						
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					(C)		HYPO	THE:	[[CA]	<u>ن</u> : _							
			(iii	i)	ORIG	INAI	SOL	JRCE	HIV:	7							
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20			(41)	ii)	SEQU	)ENCI	s Das	JUNI.	. 1101	••							
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	Сув	Thr	Arg	Pro	Ser	Asn	Asn	Thr	Arg	Lys	Ser	lle	His	lle	Ala		
	TGC	ACA	AGG	CCC	AGC	AAC	AAT	AUA	AGA	AAA	AGT	AIA	CAT	AIA	GUA		
30	•				20					25					30		
	Pro	C1 v	Are	A1a	Phe	Tvr	Thr	Thr	G1 v		Ile	Thr	G1v	Asp			
	CCA	GGG	AGA	GCA	TTT	TAT	ACA	ACA	GGA	GCA	ATA	ACA	GGA	GAT	ATA		
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	AGA	CAA	GCA	CAT	TGT												
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			(1)		(A)	المالا		GTH:	10		٠.						
					(B)				Nucl	_	Acid						
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		(ii)	KIND (if peptide or protein):  (A) SEQUENCE ASSEMBLY METHOD: Overlap  (B) FRAGMENT TYPE: Internal Fragment  (C) HYPOTHETICAL:
5		(iii)	ORIGINAL SOURCE: HIV
			(E) INDIVIDUAL ISOLATE:
		(iv)	IMMEDIATE SOURCE: (C) CLONE:
0		(v)	POSITION IN GENOME: Within Env Gene
U		(vi)	PROPERTIES OF SEQUENCE: Expresses conserved antigenic
			determinant
		(viii)	SEQUENCE DESCRIPTION:
15	SEQ ID	NO: EE3	60-3
	1 _		5 10 15 15 Ale
20	Cys Thr	Arg Pro	Ser Asn Asn Thr Arg Lys Ser Ile His Ile Ala AGC AAC AAT ACA AGA AAA AGT ATA CAT ATA GCA
	100 1101		
			20 25 30
	Pro Glw	Are Ala	Phe Tyr Thr Thr Gly Ala Ile Thr Gly Asp Ile
25	CCA GGG	AGA GCA	TTT TAT ACA ACA GGA GCA ATA ACA GGA GAT ATA
			•
			35
	Arg Gln	Ala His	Cys
30	AGA CAA	GCA CAT	TGT
	(2)		TION FOR SEQ ID NO: EE367-1
35		(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 105
			(B) TYPE: Nucleic Acid
			(C) STRANDEDNESS: Single
		<b>(</b> )	(D) TOPOLOGY: Linear
40		(ii) (ii)	KIND: cDNA to genomic RNA KIND (if peptide or protein):
		(11)	(A) SEQUENCE ASSEMBLY METHOD: Overlap
			(B) FRAGMENT TYPE: Internal Fragment
	•		(C) HYPOTHETICAL:
45		(iii)	ORIGINAL SOURCE: HIV
		(iv)	(E) INDIVIDUAL ISOLATE:
		(17)	(C) CLONE:
		(v)	POSITION IN GENOME: Within Env Gene
50		(vi)	PROPERTIES OF SEQUENCE: Expresses conserved antigenic
50		(111)	determinant
		(viii)	SEQUENCE DESCRIPTION:

SEQ ID NO: EE367-1

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5	1 Cys TGT	Thr ACA	Arg AGA	Pro CCC	5 Asn AAC	Asn AAC	Asn AAT	Thr ACA	Ile ATA	10 Lys AAA	Ser AGT	Ile ATA	His CAT	met atg	15 Gly GGA	
10	Leu CTA	Gly GGG	Arg AGG	Thr ACA	20 Phe TTT	Tyr TAT	Thr ACA	Thr ACA	Gly GGA	25 Glu GAA	Val GTA	Ile ATA	Gly GGA	Asp GAT	30 Ile ATA	
15	Arg AGA	Gln CAA	A1a GCA	His CAT	35 Cys TGT											
	(2)		TNE	TAMG!	CION	FOR	SEO	TD I	NO:	EE36	7–2					
20	(2)		(i)	)1/T W 2 1						STIC						
					(A)			GTH:	10	_						
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					(D)			OLOG:		Line						
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			(iv	)	IMMI (C)	EDIA	CLO	OURC:	E:							
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35			(vi		PRO	ERT	IES	OF S	EQUE	NCE:	Ex	pres	ses	cons	erved	antigenic
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			(vi	ii)	SEQ	JENCI	e de	SCRI	PTIO	N:						
40	SEQ	ID	NO:	EE3	67–2										•	
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	Leu Glv	Arg Thr	Phe Tyr Thr Thr Gly Glu Val Ile Gly Asp Ile	
	CTA GGG	AGG ACA	TTT TAT ACA ACA GGA GAA GTA ATA GGA GAT ATA	
_	0111 000			
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			35	
	Are Gin	Ala His		
	AGA CAA	GCA CAT	TGT	
			$\cdot$	
10				
	(2)	INFORMA'	TION FOR SEQ ID NO: EE367-3	
	<b>\-</b> /	(i)	SEQUENCE CHARACTERISTICS:	
		• •	(A) LENGTH: 105	
			(B) TYPE: Nucleic Acid	
15			(C) STRANDEDNESS: Single	
			(D) TOPOLOGY: Linear	
		(ii)	KIND: cDNA to genomic RNA	
		(ii)	KIND (if peptide or protein):	
			(A) SEQUENCE ASSEMBLY METHOD: Overlap	
20			(B) FRACMENT TYPE: Internal Fragment	
			(C) HYPOTHETICAL:	
		(iii)	ORIGINAL SOURCE: HIV	
			(E) INDIVIDUAL ISOLATE:	
-		(iv)	IMMEDIATE SOURCE:	
25			(C) CLONE:	
		(v)	POSITION IN GENOME: Within Env Gene	nic
•		(vi)	PROPERTIES OF SEQUENCE: Expresses conserved antiger	ııc
			determinant	
30		(viii)	SEQUENCE DESCRIPTION:	
30				
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	SEQ ID	NO: EE3	167–3	
35			r 10 15	
-	1		5 10	
	Cys Th	r Arg Pro	Asn Asn Asn Thr Ile Lys Ser Ile His MET Gly	
	TGT AC	A AGA CCC	C AAC AAC AAT ACA ATA AAA AGT ATA CAT ATG GGA	
40			25 30	
-			20 25	
	Leu G1	y Arg Thi	Phe Tyr Thr Thr Gly Glu Val Ile Gly Asp Ile	
	CTA GG	G AGG ACA	A TIT TAT ACA ACA GGA GAA GTA ATA GGA GAT ATA	
45			ar	
-			35	
		n Ala Hi		
	AGA CA	A GCA CA	r tgt	

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 (B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single (D) TOPOLOGY: Linear (ii) KIND: cDNA to genomic RNA (ii) KIND (if peptide or protein): (A) SEQUENCE ASSEMBLY METHOD: Overlap (B) FRACMENT TYPE: Internal Fragment (C) HYPOTHETICAL: (iii) ORIGINAL SOURCE: HIV (B) INDIVIDUAL ISOLATE: (iv) HYMEDIATE SOURCE: (C) CLONE: (v) POSITION IN GENOME: Within Env Gene (vi) PROPERTIES OF SEQUENCE: Expresses conserved antige determinant (viii) SEQUENCE DESCRIPTION:  SEQ ID NO: EE370-1  20  20  20  20  25  30  Pro Cly Arg Ala Phe Tyr Thr Thr Cly Asp Ile Ile Gly Asp Ile CCA GGA AGA GCA TTT TAT ACA ACA GCA GAC ATA ATA GGA GAT ATA  35  Arg Gln Ala His Cys AGA CAA GCA CAT GGT  40  (2) INFORMATION FOR SEQ ID NO: EE370-2 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 (B) TYPE: Nucleic Acid (C) STRANDEBNESS: Single (D) TOPOLOGY: Linear		(2)		INF	ORMA'	CION	FOR	SEQ	ID 1	NO: 1	EE37(	)–1	11.	:	Al :		21.	٠.٠.
(B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single (D) TOPOLOGY: Linear (ii) KIND: cDNA to genomic RNA (ii) KIND (if peptide or protein): (A) SEQUENCE ASSEMBLY METHOD: Overlap (B) FRAGMENT TYPE: Internal Fragment (C) HYPOTHETICAL: (iii) ORIGINAL SOURCE: HIV (E) INDIVIDUAL ISOLATE: (iv) IMMEDIATE SOURCE: (C) CLONE: (V) POSITION IN GENOME: Within Env Gene (vi) PROPERTIES OF SEQUENCE: Expresses conserved antige determinant (viii) SEQUENCE DESCRIPTION:  SEQ ID NO: EE370-1  25 1 5 10 15 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly TGT ACA ACA ACC AAC AAT ACA ACA ACA AAA ACT ATA CAT ATA GCA  30 20 25 30 Pro Cly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile CCA GGA AGA GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA  35 Arg Cln Ala His Cys AGA CAA GCA CAT TGT  40 (2) INFORMATION FOR SEQ ID NO: EE370-2 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 (B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single (D) TOPOLOGY: Linear				(i)		SEQU	JENCI	E CHA	ARAC'	Ter i	STIC	3:			•			
(C) STRANDEDNESS: Single (D) TOPOLOGY: Linear (ii) KIND: cDNA to genomic RNA (ii) KIND (if peptide or protein): (A) SEQUENCE ASSEMBLY METHOD: Overlap (B) FRAGMENT TYPE: Internal Fragment (C) HYPOTHETICAL: (iii) ORIGINAL SOURCE: HIV (E) INDIVIDUAL ISOLATE: (iv) IMMEDIATE SOURCE: (C) CLONE: (v) POSITION IN GENOME: Within Env Gene (vi) PROFERTIES OF SEQUENCE: Expresses conserved antige determinant (viii) SEQUENCE DESCRIPTION:  SEQ ID NO: EE370-1  25  1 5 10 15 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA  36  20  20  25  30  Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile CCA GGA AGA GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA  37  38  39  20  20  25  30  Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile CCA GGA AGA GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA  36  37  38  49  40  (2) INFORMATION FOR SEQ ID NO: EE370-2 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 (B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single (D) TOPOLOGY: Linear						(A)		LEN	GTH:	10	5				•			•
(C) STRANDENESS: SINGLE  (D) TOPOLOGY: Linear  (ii) KIND: cDNA to genomic RNA  (ii) KIND (if peptide or protein):  (A) SEQUENCE ASSEMBLY METHOD: Overlap  (B) FRAGMENT TYPE: Internal Fragment (C) HYPOTHETICAL:  (iii) ORIGINAL SOURCE: HIV  (B) INDIVIDUAL ISOLATE:  (iv) IMMEDIATE SOURCE:  (c) CLONE:  (v) POSITION IN GENOME: Within Env Gene (vi) PROPERTIES OF SEQUENCE: Expresses conserved antiged determinant (viii) SEQUENCE DESCRIPTION:  SEQ ID NO: EE370-1  SEQ ID NO: EE370-1  20  Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile CCA GGA AGA GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA  35  Arg Gln Ala His Cys AGA CAA GGA GAC ATA ATA GGA GAT ATA  36  37  Arg Gln Ala His Cys AGA CAA CAA CAA CAA CAA CAA CAA CAA CAA						(B)		TYP	B: 1	Nucl	eic A	Acid	•					
(ii) KIND: cDNA to genomic RNA (ii) KIND (if peptide or protein): (A) SEQUENCE ASSEMBLY METHOD: Overlap (B) FRAGMENT TYPE: Internal Fragment (C) HYPOTHETICAL: (iii) ORIGINAL SOURCE: HIV (E) INDIVIDUAL ISOLATE: (iv) IMMEDIATE SOURCE: (C) CLONE: (v) POSITION IN GENOME: Within Env Gene (vi) PROPERTIES OF SEQUENCE: Expresses conserved antiged determinant (viii) SEQUENCE DESCRIPTION:  SEQ ID NO: EE370-1  20 SEQ ID NO: EE370-1  25 1 5 10 15 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA  30 Pro Gly Arg Ala Phe Tyr Thr Thr Cly Asp Ile Ile Gly Asp Ile CCA GGA AGA GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA  35 Arg Gln Ala His Cys AGA CAA GCA CAT TGT  40 (2) INFORMATION FOR SEQ ID NO: EE370-2 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 (B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single (D) TOPOLOGY: Linear	5					(C)		STR	ANDE	DNES	S: S	Sing	le .					
(ii) KIND: cDNA to genomic RNA (ii) KIND (if peptide or protein): (A) SEQUENCE ASSEMBLY METHOD: Overlap (B) FRAGMENT TYPE: Internal Fragment (C) HYPOTHETICAL: (iii) ORIGINAL SOURCE: HIV (E) INDIVIDUAL ISOLATE: (iv) IMMEDIATE SOURCE: (C) CLONE: (v) POSITION IN GENOME: Within Env Gene (vi) PROPERTIES OF SEQUENCE: Expresses conserved antiged determinant (viii) SEQUENCE DESCRIPTION:  SEQ ID NO: EE370-1  20 SEQ ID NO: EE370-1  25 1 5 10 15 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA  30 Pro Gly Arg Ala Phe Tyr Thr Thr Cly Asp Ile Ile Gly Asp Ile CCA GGA AGA GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA  35 Arg Gln Ala His Cys AGA CAA GCA CAT TGT  40 (2) INFORMATION FOR SEQ ID NO: EE370-2 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 (B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single (D) TOPOLOGY: Linear								TOP	DLOG	Y: :	Linea	ar Č			;	•		
(ii) KIND (if peptide or protein):  (A) SEQUENCE ASSEMBLY METHOD: Overlap  (B) FRAGMENT TYPE: Internal Fragment  (C) HYPOTHETICAL:  (iii) ORIGINAL SOURCE: HIV  (B) INDIVIDUAL ISOLATE:  (iv) IMMEDIATE SOURCE:  (C) CLONE:  (v) POSITION IN GENOME: Within Env Cene  (vi) PROPERTIES OF SEQUENCE: Expresses conserved antiged determinant  (viii) SEQUENCE DESCRIPTION:  SEQ ID NO: EE370-1  SEQ ID NO: EE370-1  25  1  5  10  15  Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly TGT ACA ACA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA  30  20  20  25  30  Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile CCA GGA AGA GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA  35  Arg Gln Ala His Cys AGA CAA GCA CAT TGT  40  (2) INFORMATION FOR SEQ ID NO: EE370-2  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 105  (B) TYPE: Nucleic Acid  (C) STRANDEDNESS: Single  (D) TOPOLOGY: Linear				(ii)	)		D: cl											
(A) SEQUENCE ASSEMBLY METHOD: Overlap (B) FRAGMENT TYPE: Internal Fragment (C) HYPOTHETICAL: (iii) ORIGINAL SOURCE: HIV (E) INDIVIDUAL ISOLATE: (iv) HMMEDIATE SOURCE: (C) CLONE: (V) POSITION IN GENOME: Within Env Gene (vi) PROPERTIES OF SEQUENCE: Expresses conserved antige determinant (viii) SEQUENCE DESCRIPTION:  SEQ ID NO: EE370-1  SEQ ID NO: EE370-1  25  1 5 10 15 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA  30  Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile CCA GGA AGA GCA TTT TAT ACA AGA GGA GAC ATA ATA GGA GAT ATA  35  Arg Gln Ala His Cys AGA CAA GCA CAT TGT  40  (2) INFORMATION FOR SEQ ID NO: EE370-2 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 (B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single (D) TOPOLOGY: Linear													):	-				
(B) FRAGMENT TYPE: Internal Fragment (C) HYPOTHETICAL: (iii) ORIGINAL SOURCE: BIV (E) INDIVIDUAL ISOLATE: (iv) IMMEDIATE SOURCE: (C) CLONE: (V) POSITION IN GENOME: Within Env Gene (vi) PROPERTIES OF SEQUENCE: Expresses conserved antige determinant (viii) SEQUENCE DESCRIPTION:  SEQ ID NO: EE370-1  SEQ ID NO: EE370-1  25 1 5 10 15 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA  30 20 25 30 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile CCA GGA AGA GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA  35 Arg Gln Ala His Cys AGA CAA GCA CAT TGT  40 (2) INFORMATION FOR SEQ ID NO: EE370-2 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 (B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single (D) TOPOLOGY: Linear				,,	•		• •							D: (	Over:	lap		
(C) HYPOTHETICAL: (iii) ORIGINAL SOURCE: BIV (E) INDIVIDUAL ISOLATE: (iv) HYMEDIATE SOURCE: (C) CLONE: (V) POSITION IN GENOME: Within Env Gene (vi) PROPERTIES OF SEQUENCE: Expresses conserved antige determinant (viii) SEQUENCE DESCRIPTION:  SEQ ID NO: EE370-1  SEQ ID NO: EE370-1  25  1  5  10  15  Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA  30  20  20  25  30  Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile CCA GGA AGA GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA  35  Arg Gln Ala His Cys AGA CAA GCA GCA GAC ATA ATA GGA GAT ATA  40  (2) INFORMATION FOR SEQ ID NO: EE370-2 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 (B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single (D) TOPOLOGY: Linear	10					,		•									•	
(iii) ORIGINAL SOURCE: HIV (E) INDIVIDUAL ISOLATE: (iv) IMMEDIATE SOURCE: (C) CLONE: (v) POSITION IN GENOME: Within Env Gene (vi) PROPERTIES OF SEQUENCE: Expresses conserved antige determinant (viii) SEQUENCE DESCRIPTION:  SEQ ID NO: EE370-1  25 1 5 10 15 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA  30 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile CCA GGA AGA GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA  35 Arg Gln Ala His Cys AGA CAA GCA CAT TGT  40 (2) INFORMATION FOR SEQ ID NO: EE370-2 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 (B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single (D) TOPOLOGY: Linear																		
(E) INDIVIDUAL ISOLATE:  (iv) IMMEDIATE SOURCE:  (C) CLONE:  (v) POSITION IN GENOME: Within Env Gene  (vi) PROPERTIES OF SEQUENCE: Expresses conserved antige determinant  (viii) SEQUENCE DESCRIPTION:  SEQ ID NO: EE370-1  25 1 5 10 15  Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA  30 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile CCA GGA AGA GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA  35 Arg Gln Ala His Cys AGA CAA GCA CAT TGT  40 (2) INFORMATION FOR SEQ ID NO: EE370-2  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 105  (B) TYPE: Nucleic Acid  (C) STRANDEDNESS: Single  (D) TOPOLOGY: Linear				(iii	i )		CTNA	-	-		-		-					
(iv) IMMEDIATE SOURCE: (C) CLONE: (v) POSITION IN GENOME: Within Env Gene (vi) PROPERTIES OF SEQUENCE: Expresses conserved antige determinant (viii) SEQUENCE DESCRIPTION:  SEQ ID NO: EE370-1  SEQ ID NO: EE370-1  25  1  Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA  30  Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile CCA GGA AGA GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA  35  Arg Gln Ala His Cys AGA CAA GCA CAT TGT  40  (2) INFORMATION FOR SEQ ID NO: EE370-2 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 (B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single (D) TOPOLOGY: Linear				\	-,							ATE:						_
(C) CLONE:  (v) POSITION IN GENOME: Within Env Gene (vi) PROPERTIES OF SEQUENCE: Expresses conserved antige determinant (viii) SEQUENCE DESCRIPTION:  SEQ ID NO: EE370-1  25 1 5 10 15 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA  30 20 25 30 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile CCA GGA AGA GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA  35 35 Arg Gln Ala His Cys AGA CAA GCA CAT TGT  40 (2) INFORMATION FOR SEQ ID NO: EE370-2 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 (B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single 45 (D) TOPOLOGY: Linear				(iv	)	,	RDTA'											
(v) POSITION IN GENOME: Within Env Gene (vi) PROPERTIES OF SEQUENCE: Expresses conserved antige determinant (viii) SEQUENCE DESCRIPTION:  SEQ ID NO: EE370-1  SEQ ID NO: EE370-1  25  1  5  Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA  30  Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile CCA GGA AGA GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA  35  Arg Gln Ala His Cys AGA CAA GCA CAT TGT  40  (2) INFORMATION FOR SEQ ID NO: EE370-2 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 (B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single (D) TOPOLOGY: Linear	15			(	•					_ `								
(vi) PROPERTIES OF SEQUENCE: Expresses conserved antige determinant (viii) SEQUENCE DESCRIPTION:  SEQ ID NO: EE370-1  SEQ ID NO: EE370-1  25  1  Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA  30  Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile CCA GGA AGA GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA  35  Arg Gln Ala His Cys AGA CAA GCA CAT TGT  40  (2) INFORMATION FOR SEQ ID NO: EE370-2 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 (B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single (D) TOPOLOGY: Linear				(v)			TTTO			OME:	Wit	hin l	Env (	Gene	_			
determinant (viii) SEQUENCE DESCRIPTION:  SEQ ID NO: EE370-1  25					_										cons	erve	d anti	lgenic
SEQ ID NO: EE370-1  25  1  5  Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA  30  Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile CCA GGA AGA GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA  35  Arg Gln Ala His Cys AGA CAA GCA CAT TGT  40  (2) INFORMATION FOR SEQ ID NO: EE370-2  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 105  (B) TYPE: Nucleic Acid  (C) STRANDEDNESS: Single  45  45				( • -	,					-4								
SEQ ID NO: EE370-1  25  1 5 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA  30 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile CCA GGA AGA GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA  35 Arg Gln Ala His Cys AGA CAA GCA CAT TGT  40 (2) INFORMATION FOR SEQ ID NO: EE370-2 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 (B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single 45  45				(wi	i i )				SCRI	PTIO	<b>V</b> :			<i>,</i>				
SEQ ID NO: EE370-1  25  1 5 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA  30 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile CCA GGA AGA GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA  35 Arg Gln Ala His Cys AGA CAA GCA CAT TGT  40 (2) INFORMATION FOR SEQ ID NO: EE370-2 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 (B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single 45  45	20			( • 1.	LI	SEQ	013101	יטעט	JOIL .	110	•				٠.			
25 1 5 10 15 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA  30 20 25 30 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile CCA GGA AGA GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA  35 Arg Gln Ala His Cys AGA CAA GCA CAT TGT  40 (2) INFORMATION FOR SEQ ID NO: EE370-2 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 (B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single 45 45													٠,	•				
25 1 5 10 15 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA  30 20 25 30 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile CCA GGA AGA GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA  35 Arg Gln Ala His Cys AGA CAA GCA CAT TGT  40 (2) INFORMATION FOR SEQ ID NO: EE370-2 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 (B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single 45 45		SEO	ו מז	vn•	EE3	70-1												
Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA  20 25 30 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile CCA GGA AGA GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA  35 Arg Gln Ala His Cys AGA CAA GCA CAT TGT  40 (2) INFORMATION FOR SEQ ID NO: EE370-2 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 (B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single 45		buq	10.															
Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA  20 25 30 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile CCA GGA AGA GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA  35 Arg Gln Ala His Cys AGA CAA GCA CAT TGT  40 (2) INFORMATION FOR SEQ ID NO: EE370-2 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 (B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single 45																		
Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA  20 25 30  Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile CCA GGA AGA GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA  35  Arg Gln Ala His Cys AGA CAA GCA CAT TGT  40  (2) INFORMATION FOR SEQ ID NO: EE370-2 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 (B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single 45	25	1				5					10					15		
TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA  20 25 30 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile CCA GGA AGA GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA  35 Arg Gln Ala His Cys AGA CAA GCA CAT TGT  40 (2) INFORMATION FOR SEQ ID NO: RE370-2 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 (B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single 45			Thr	Aro	Pro	-	Asn	Asn	Thr	Arg		Ser	I1e	His	Ile	G1v	÷	
20 25 30  Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile CCA GGA AGA GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA  35  Arg Gln Ala His Cys AGA CAA GCA CAT TGT  40  (2) INFORMATION FOR SEQ ID NO: EE370-2  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 105  (B) TYPE: Nucleic Acid  (C) STRANDEDNESS: Single  45  (D) TOPOLOGY: Linear		тст	ACA	AGA	CCC	AAC	AAC	AAT	ACA	AGA	AAA	AGT	ATA	CAT	ATA	GGA		
Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile CCA GGA AGA GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA  35  Arg Gln Ala His Cys AGA CAA GCA CAT TGT  40  (2) INFORMATION FOR SEQ ID NO: EE370-2  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 105  (B) TYPE: Nucleic Acid  (C) STRANDEDNESS: Single  45  (D) TOPOLOGY: Linear		101	ANCA	11011	000		****											
Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile CCA GGA AGA GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA  35  Arg Gln Ala His Cys AGA CAA GCA CAT TGT  40  (2) INFORMATION FOR SEQ ID NO: EE370-2  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 105  (B) TYPE: Nucleic Acid  (C) STRANDEDNESS: Single  45  (D) TOPOLOGY: Linear																		
Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile CCA GGA AGA GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA  35  Arg Gln Ala His Cys AGA CAA GCA CAT TGT  40  (2) INFORMATION FOR SEQ ID NO: EE370-2 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 (B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single 45  (D) TOPOLOGY: Linear	30					20					25				•	30		•
CCA GGA AGA GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA  35  Arg Gln Ala His Cys AGA CAA GCA CAT TGT  40  (2) INFORMATION FOR SEQ ID NO: EE370-2 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 (B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single 45  (D) TOPOLOGY: Linear		Pro	C1 v	Ara	A1a		Tvr	Thr	Thr	G1 v		Tle	Ile	G1 v	Asp	Ile		
35 Arg Gln Ala His Cys AGA CAA GCA CAT TGT  40 (2) INFORMATION FOR SEQ ID NO: EE370-2 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 (B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single 45 (D) TOPOLOGY: Linear		CCA	CCA	AGA	GCA	TTT	TAT	ACA	ACA	GGA	GAC	ATA	ATA	GGA	GAT	ATA		
Arg Gln Ala His Cys AGA CAA GCA CAT TGT   40 (2) INFORMATION FOR SEQ ID NO: EE370-2 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 (B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single 45 (D) TOPOLOGY: Linear		0011		1.011						7		,						
Arg Gln Ala His Cys AGA CAA GCA CAT TGT   40 (2) INFORMATION FOR SEQ ID NO: EE370-2 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 (B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single 45 (D) TOPOLOGY: Linear																		
Arg Gln Ala His Cys AGA CAA GCA CAT TGT   40 (2) INFORMATION FOR SEQ ID NO: EE370-2 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 (B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single 45 (D) TOPOLOGY: Linear	35					35												
AGA CAA GCA CAT TGT  40 (2) INFORMATION FOR SEQ ID NO: EE370-2 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 (B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single 45 (D) TOPOLOGY: Linear		Ara	G1n	A1s	Hic													
40 (2) INFORMATION FOR SEQ ID NO: EE370-2 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 (B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single 45 (D) TOPOLOGY: Linear	,																	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 105  (B) TYPE: Nucleic Acid  (C) STRANDEDNESS: Single  (D) TOPOLOGY: Linear		II.CA1	OLM.	ou.	0411											•		•
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 105  (B) TYPE: Nucleic Acid  (C) STRANDEDNESS: Single  (D) TOPOLOGY: Linear																		
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 105  (B) TYPE: Nucleic Acid  (C) STRANDEDNESS: Single  (D) TOPOLOGY: Linear	40	(2)		INF	ORMA'	TION	FOR	SEO	TD :	NO:	RE37	0-2						
(A) LENGTH: 105 (B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single (D) TOPOLOGY: Linear		(-)														•		
(B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single (D) TOPOLOGY: Linear				(1)		•						- •						
(C) STRANDEDNESS: Single (D) TOPOLOGY: Linear											-	hioA						
45 (D) TOPOLOGY: Linear												_	-					-
(D) TOPOLOGI: Linear	45											_	<b>-</b> C					
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			(iv)		IMME (C)		CLO										
10			(v) (vi)		PROF		ES (					Env ( press		cons	erved	antige	enic
			(vi	ii)				SCRI	PTION	<b>1:</b>							
15	SEQ	ID 1	10:	EE37	70–2												
	1				5					10					15		
20	Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile	His	Ile	Gly		
20	TGT	ACA	AGA	CCC	AAC	AAC	AAT	ACA	AGA	AAA	AGT	ATA	CAT	ATA	, GGA		
					20					25					30		
	Dwa	C1	A =	410	20 Pho	Тиг	Thr	Thr	G1 w		T10	Tle	G1 w	Agn	Ile		
25	CCA	GGA	AGA	GCA	TTT	TAT	ACA	ACA	GGA	GAC	ATA	ATA	GGA	GAT	ATA		
					25												
	A 2	01-	41-	11.1	35												
30	_		Ala GCA														
	non	OLM'	5011	· · · · ·	101												
	(2)			ORMA:					NO:								
35			(i)		SEQUAL (A)			akaç GTH:	TER I:		5:						
					(B)		TYP		Nuc1		Acid						
					(c)				DNES		Sing	le					
					(D)			OLOG		Line							
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					(c)				TICA								
			(ii	i)			L SO	URCE	: HI	♥ .						•	
<b>4</b> 5					(E)				UAL	ISOL	ATE:						
			(iv	)				OURC	E:								
			(v)		(C)		CLO N TN		OMF •	Wit	hin	Env	Gene	-			
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50			, • 1	•		ermi											
		•	(vi	ii)					PTIO	N:							

SEO ID NO: EE370-3

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10 5 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA 30 20 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile 10 CCA GGA AGA GCA TIT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA Arg Gln Ala His Cys AGA CAA GCA CAT TGT INFORMATION FOR SEQ ID NO: EE374-1 (2) SEQUENCE CHARACTERISTICS: 20 (i) LENGTH: 105 (A) TYPE: Nucleic Acid (B) STRANDEDNESS: Single (C) (D) TOPOLOGY: Linear KIND: cDNA to genomic RNA 25 (ii) (ii) KIND (if peptide or protein): SEQUENCE ASSEMBLY METHOD: Overlap (A) (B) FRACMENT TYPE: Internal Fragment (C) HYPOTHETICAL: ORIGINAL SOURCE: HIV 30 (iii) INDIVIDUAL ISOLATE: IMMEDIATE SOURCE: (iv) (C) CLONE: POSITION IN GENOME: Within Env Gene (v) PROPERTIES OF SEQUENCE: Expresses conserved antigenic (vi) 35 determinant SEQUENCE DESCRIPTION: (viii) SEQ ID NO: EE374-1 10

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Cys Ile Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly TGT ATA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

			20
	D C1-	. Ama Ala	20 25 30 Phe Tyr Thr Thr Gly Thr Ile Ile Gly Asp Ile
	CCA CCC	ACA GCA	TIT TAT ACA ACA GGA ACA ATA ATA GGA GAT ATA
	001 000	11011 0011	
5			
			35
	_	Ala His	· ·
	AGA CAA	GCA CAT	TGT
10			
	(2)	INFORMA	TION FOR SEQ ID NO: EE374-2
	(-/	(i)	SEQUENCE CHARACTERISTICS:
			(A) LENGTH: 105
15			(B) TYPE: Nucleic Acid
			(C) STRANDEDNESS: Single
		(22)	(D) TOPOLOGY: Linear KIND: cDNA to genomic RNA
		(ii) (ii)	KIND (if peptide or protein):
		(11)	(A) SEQUENCE ASSEMBLY METHOD: Overlap
20			(B) FRAGMENT TYPE: Internal Fragment
			(C) HYPOTHETICAL:
		(iii)	ORIGINAL SOURCE: HIV
		(4)	(E) INDIVIDUAL ISOLATE:
25		(iv)	(C) CLONE:
		(v)	POSITION IN GENOME: Within Env Gene
		(iv)	PROPERTIES OF SEQUENCE: Expresses conserved antigenic
			determinant
30	-	(viii)	SEQUENCE DESCRIPTION:
	CPO ID	NO. PP2	74–2
	SEQ ID	NO. ESJ	74-2
35	1		5 10 15
33	Cys Ile	Arg Pro	Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly
	TGT ATA	AGA CCC	AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA
			20 25 30
40	Pro Gly	Arg Ala	Phe Tyr Thr Thr Gly Thr Ile Ile Gly Asp Ile
	CCA GGG	AGA GCA	TTT TAT ACA ACA GGA ACA ATA ATA GGA GAT ATA
			35
45	Arg Gln	Ala His	
ì	•	GCA CAT	

	(2)		INF	ORMA:	LION	FOR	SEQ	ID I	NO: 1	EE374	4-3					
			(i)		SEQ	UENC	E CH	ARAC'	TERI:	STIC	S:					
					(A)		LEN	GTH:	10:	5						
					(B)		TYP	E: ]	Nucl	eic A	Acid					
5					(C)		STR	ANDE	DNES:	s: s	Sing	le				
					(D)		TOP	OLOG:	Y: 1	Line	ar					
			(ii	)	KIN	D: cl	DNA	to go	enom:	ic R	A					
			(ii	)	KIN	D (i		ptid								
					(A)		SEQ	UENC	E AS	SEMB!						
10					(B)		FRA	GMEN.	r TY	PE:	Inte	erna	l Fra	agme	at	
					(C)			OTHE:		-						
		•	(ii	i)				URCE								
					(E)			IVID		ISOL	ATE:					
			(iv	)		EDIA:		OURC	E:							
15					(C)		CLO							-		
			(v)	_				GEN								
			(vi	)				OF S	EQUE	NCE:	Ex	pres	ses (	cons	erved	antigenic
			, .			ermi										•
20			(vi	11)	SEQ	UENC	R DE	SCRI	PTIO	N:						
	SEQ	ID 1	NO:	EE3	74–3											•
25	1				5					10					15	
	Cys	Ile	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile	His	Ile	Gly	•
	TGT	ATA	AGA	CCC	AAC	AAC	AAT	ACA	AGA	AAA	AGT	ATA	CAT	ATA	GGA	
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30										0.5					20	
30	_				20		-	· · · ·	<b>01</b> -	25	T1 -	71 -	<b>01</b>	A	30	
	Pro	GLY	Arg	ALA	rne	lyr	Inr	Thr	GIA	Inr	TIE	116	GIY	ASP	116	
	CCA	GGG	AGA	GCA	TIT	TAT	AUA	AÇA	GGA	AUA	AIA	AIA	GGA	GAI	AIM	
35					35											
	Ara	G1n	A1 a	His												
	_			CAT	-											
		01.11	0011	0111												
40	(2)		INF	ORMA:	TION	FOR	SEQ	ID I	NO:	EE37	8–1					
			(i)					ARAC'						•		
					(A)		LEN	GTH:	10	5						
					(B)		TYP	<b>E:</b> ]	Nucl	eic	Acid					
					(C)		STR	ANDE	DNES	S:	Sing	1e				
45					(D)		TOP	OLOG	Y: :	Line	ar					
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			(ii)	)	KINI				e or								
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5					(C)				[[CA]	_							
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		The	A=~	Pro	Asn	Aen	Acn	Thr	Ara		Ser	T10	Hio	T1e			
20					AAC												
	101	11011		000	1110								<b></b>				
					20					25					30		
25	Pro	Gly	Arg	Ala	Phe	Tyr	Thr	Thr	G1y	G1u	I1e	Ile	G1y	Asp	Ile		
	CCA	GGG	AGA	GCA	TTT	TAT	ACA	ACA	GGA	GAA	ATA	ATA	GGA	GAT	ATA		
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50			\ <b>*</b> ±	,		ermi		J. D.	~40m			F- 40		HD	v u	, cureage	
			(vi	11)	SEO			SCRT	PTTO	N:							

SEQ ID NO: EE378-2 10 1 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly 5 TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA 30 25 20 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asp Ile 10 CCA GGG AGA GCA TIT TAT ACA ACA GGA GAA ATA ATA GGA GAT ATA 35 Arg Gln Ala His Cys AGA CAA GCA CAT TGT INFORMATION FOR SEQ ID NO: EE378-3 (2) SEQUENCE CHARACTERISTICS: 20 (i) LENGTH: 105 (A) TYPE: Nucleic Acid (B) STRANDEDNESS: Single (C) TOPOLOGY: Linear (D) KIND: cDNA to genomic RNA 25 (ii) KIND (if peptide or protein): (ii) SEQUENCE ASSEMBLY METHOD: Overlap (A) FRAGMENT TYPE: Internal Fragment (B) (C) HYPOTHETICAL: ORIGINAL SOURCE: HIV 30 (iii) INDIVIDUAL ISOLATE: (E) IMMEDIATE SOURCE: (iv) CLONE: (C) POSITION IN GENOME: Within Env Gene (v) PROPERTIES OF SEQUENCE: Expresses conserved antigenic 35 (vi) determinant (viii) SEQUENCE DESCRIPTION: 40 SEQ ID NO: EE378-3

1 5 10 15
Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Pro Ile Gly
TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CCT ATA GGA

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					20					25					30		
	_	n1	<b>.</b>	A1	Pho	Ture	Thir	Thr	Gly	Glu i	[le	Ile	G1y	Asp	Ile		
	Pro	er <b>y</b>	Arg	MIN	THE	TAT	ACA	ACA	GGA (	GAA	ATA	ATA	GGA	GAT	ATA		
	CCA	فافاق	AGA	GUA	111	TVT	M	21041									
5																	
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	Arg AGA	GIN	BLA	UIR	TOT												
	AGA	CAA	GUA	CMI	161												
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	(0)		TME	DMA?	rto <b>n</b>	FOR	SEO	ID I	10: E	E380	-1						
	(2)		(i)	)MIN.	CEUI	IFNC	E CH	ARAC'	rer is	TICS	:						
			(1)		(A)			GTH:									
					(B)		TYP	E: ]	Nucle		cid						
15					(c)		STR	ANDE	DNESS	: S	ingl	.e					
					(D)				Y: L								
			(ii	`	KIN	): c	DNA	to g	enomi	c RN	Α						
			(ii		KIN	) (i	f · pe	ntid	e or	prot	ein)	:					
			(11	,	(A)		SEO	UENC	E ASS	EMBL	Y ME	THOI	D:	0ver	lap		
20					(B)		FRA	GMEN	T TYP	E:	Inte	rna	L Fr	agme	ent		
					(c)		HYP	OTHE	TICAI								
			(ii	4)	ORT	CTNA			: HIV								
			(11	_,	(E)		INI	IVID	UAL 1	SOLA	TE:						
			(iv	)	LMM	KDTV	16 5	UURU	D.								
25			(iv	)	(c)		CLC	OURC NE:						<u></u>			
25					(C)	TTTC	CLC N TN	NE:	OME:	With	nin l	3nv	Gene	<u></u>		*	
25			(v)		(C)	TTTC	CLC N TN	NE:	OME:	With	nin l Exp	Snv pres	Gene ses	con	served	antig	enic
25					(C) POS PRO det	ITIC PERI ermi	CLC N IN IES nant	NE: Gen Of S	OME: EQUE	MCE:	in l Exp	inv pres	Gene ses	con	served	antig	enic
			(v) (vi	)	(C) POS PRO det	ITIC PERI ermi	CLC N IN IES nant	NE: Gen Of S	OME: EQUE	MCE:	in l Exp	Snv pres	Gene ses	CODE	served	antig	enic
25			(v) (vi		(C) POS PRO det	ITIC PERI ermi	CLC N IN IES nant	NE: Gen Of S	OME:	MCE:	in l Exp	Snv pres	Gene ses	CODE	served	antig	enic
			(v) (vi	)	(C) POS PRO det	ITIC PERI ermi	CLC N IN IES nant	NE: Gen Of S	OME: EQUE	MCE:	in l Exp	Snv pres	Gene ses	cons	served	antig	enic
	SEO	ID	(v) (vi	) ii)	(C) POS PRO det SEQ	ITIC PERT ermi UENC	CLC N IN IES nant	NE: Gen Of S	OME: EQUE	MCE:	nin l Exp	Snv pres	Gene ses	cons	served	antig	enic
	SEQ	ID	(v) (vi	)	(C) POS PRO det SEQ	ITIC PERT ermi UENC	CLC N IN IES nant	NE: Gen Of S	OME: EQUE	MCE:	in l Exp	Snv pres	Gene ses	con	served	antig	enic
30	SEQ	ID	(v) (vi	) ii)	(C) POS PRO det SEQ	ITIC PERT ermi UENC	CLC N IN IES nant	NE: Gen Of S	OME: EQUE	NCE:	Exp	Env pres	Gene ses	con		antig	enic
	1		(v) (vi (vi NO:	) ii) EE3	(C) POS PRO det SEQ	ITIC PERI ermi UENC	CLC N IN PIES nant E DI	NE: I GEN OF S : ESCRI	OME: EEQUET	NCE: N: 10	Exp	pres	ses	CON	15	antig	enic
30	1	Th.	(v) (vi (vi NO:	ii) EE3	(C) POS PRO det SEQ	ITIC PERT ermi UENC	CLC N IN TIES nant E DI	NE: GEN OF S SCRI	OME: SEQUEN	NCE: N: 10 Lvs	Exp	pres Ile	ses : His	cons	15 e G1y	antig	enic
30	1	Th.	(v) (vi (vi NO:	ii) EE3	(C) POS PRO det SEQ	ITIC PERT ermi UENC	CLC N IN TIES nant E DI	NE: GEN OF S SCRI	OME: SEQUEN	NCE: N: 10 Lvs	Exp	pres Ile	ses : His	cons	15 e G1y	antigo	enic
30	1	Th.	(v) (vi (vi NO:	ii) EE3	(C) POS PRO det SEQ	ITIC PERT ermi UENC	CLC N IN TIES nant E DI	NE: GEN OF S SCRI	OME: SEQUEN	NCE: N: 10 Lvs	Exp	pres Ile	ses : His	cons	15	antigo	enic
30	1	Th.	(v) (vi (vi NO:	ii) EE3	(C) POS PRO det SEQ	ITIC PERT ermi UENC	CLC N IN TIES nant E DI	NE: GEN OF S SCRI	OME: SEQUEN	VCE: N: 10 Lys AAA	Ser AGT	pres Ile	ses : His	cons	15 e Gly A GGA	antigo	enic
30	1 Cys TGT	Thr	(v) (vi (vi NO:	ii) EE3	(C) POS PRO det SEQ 80-1	ITIC PERT ermi UENC	CLC N IN PIES nant E DI	NE: GEN OF S SSCRI	EQUET PTION	VCE: N: 10 Lys AAA	Ser AGT	Ile ATA	ses Hia CA	cons	15 e G1y A GGA	antigo	enic
30	1 Cys TGT	The	(vi (vi NO:	ii) EE3	(C) POS PRO det SEQ 80-1	ITIC PERT ermi UENC	CIAN IN INTERPORTED TO THE PROPERTY OF THE PRO	NE: GEN OF S SSCRI	OME: EQUET PTION	IO Lys AAA	Ser AGT	Ile ATA	ses His CAT	s Il	15 e Gly A GGA 30 p Ile	antigo	enic
30	1 Cys TGT	The	(vi (vi NO:	ii) EE3	(C) POS PRO det SEQ 80-1	ITIC PERT ermi UENC	CIAN IN INTERPORTED TO THE PROPERTY OF THE PRO	NE: GEN OF S SSCRI	OME: EQUET PTION	IO Lys AAA	Ser AGT	Ile ATA	ses His CAT	s Il	15 e Gly A GGA 30 p Ile	antig	enic
30	1 Cys TGT	The	(vi (vi NO:	ii) EE3	(C) POS PRO det SEQ 80-1	ITIC PERT ermi UENC	CIAN IN INTERPORT OF THE PROPERTY OF THE PROPE	NE: GEN OF S SSCRI	OME: EQUET PTION	IO Lys AAA	Ser AGT	Ile ATA	ses His CAT	s Il	15 e G1y A GGA	antig	enic
35 35	1 Cys TGT	The	(vi (vi NO:	ii) EE3	(C) POS PRO det SEQ 80-1 5 Ser AGC	ITIO PERI Ermi UENO Asi Asi AA	CIAN IN INTERPORT OF THE PROPERTY OF THE PROPE	NE: GEN OF S SSCRI	OME: EQUET PTION	IO Lys AAA	Ser AGT	Ile ATA	ses His CAT	s Il	15 e Gly A GGA 30 p Ile	antig	enic
30	1 Cys TGT Pro	Thz ACA G13 GG0	(vi (vi NO:	ii) EE3 CCC	(C) POS PRO det SEQ 80-1 5 Ser AGC	ITIO PERT ermi UENO Asi : Asi	CIAN IN INTERPORT OF THE PROPERTY OF THE PROPE	NE: GEN OF S SSCRI	OME: EQUET PTION	IO Lys AAA	Ser AGT	Ile ATA	ses His CAT	s Il	15 e Gly A GGA 30 p Ile	antig	enic
35 35	1 Cys TGT Pro CCA	Thr ACA G13 GG0	(v) (vi (vi  NO: Arg	ii) EE3 Pro	(C) POS PRO det SEQ 80-1 5 Ser AGC 20 4 Phe	ITIO PERT ermi UENO Asi : Asi	CIAN IN INTERPORT OF THE PROPERTY OF THE PROPE	NE: GEN OF S SSCRI	OME: EQUET PTION	IO Lys AAA	Ser AGT	Ile ATA	ses His CAT	s Il	15 e Gly A GGA 30 p Ile	antig	enic
35 35	1 Cys TGT Pro CCA	Thr ACA G13 GG0	(v) (vi (vi  NO: Arg	ii) EE3 CCC	(C) POS PRO det SEQ 80-1 5 Ser AGC 20 4 Phe	ITIO PERT ermi UENO Asi : Asi	CIAN IN INTERPORT OF THE PROPERTY OF THE PROPE	NE: GEN OF S SSCRI	OME: EQUET PTION	IO Lys AAA	Ser AGT	Ile ATA	ses His CAT	s Il	15 e Gly A GGA 30 p Ile	antig	enic

	(2)		INFO	RMAT	ION	FOR	SEQ	ID N	0: E	E380	-2						
*			(i)		SEQU	ENCE	CHA	RACT	ERIS	TICS	:						,
			• •		(A)		LENG	TH:	105								
					(B)		TYPE			ic A							
5					(C)		STRA	NDED	NESS	: S	ingl	е					
					(D)		TOPO	LOGY	: L	inea	r						
			(ii)	)	KIND	: cD	NA t	o ge	nomi	c RN	A						
			(ii)	)	KIND	(if	per	tide	OF	prot	ein)	:					
			•		(A)		SEQU	ENCE	ASS	EMBL	Y ME	THOD	): 0	verl	ap		
10					(B)		FRAG	MENT	TYP	E:	Inte	rnal	Fra	gmen	t		
					(C)		HYPO	THEI	CICAL	<b>:</b> _							
			(iii	i)	ORIG	INAI			HIV								
			•	•	(E)		INDI	VIDU	JAL I	SOLA	TE:						
			(iv)	)	IMME	CAIC	E SC	URCE	<b>:</b> :								
15			•		(C)		CLON							-			
			(v)		POS1	TION	IN	GEN(	ME:	With	in E	inv (	ene		_	. •	
			(vi)	)	PROF	ERT1	ES C	)F SI	QUEN	ICE:	Exp	ress	es c	conse	rved	anti	genic
						ermin											
			(vi	ii)	SEQU	JENCI	DES	SCRII	COLTS	<b>!</b> :							
20																	
	SEQ	ID ?	10:	EE38	30-2									,			
25					_					10					15		
23	1				5	_			A	10	C	TIA	ui.	Tla			
	Cys	Thr	Arg	Pro	Ser	Asn	Asn	Thr	Arg	Lys	Ser	TTE	TIB	TTE	CCA		
	TGT	ACA	AGA	CCC	AGC	AAC	AAT	ACA	AGA	AAA	MGI	WIW	OUT	MIN	GOII		
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00	_				20	m	TTL	Th.	C1++	Glu	Tie	T1e	Clv	Agn			
	Pro	Gly	Arg	Ala	rne	TAT	THE	THE	CCV	GAA	ATA	ATA	CCA	GAT	ATA		
	CCA	GGG	AGA	GCA	TTT	IAI	AUA	AUA	GGA	GUU	AIA	nın	001				
35					35												
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					Сув												
	AGA	CAA	GUA	CAI	TGT												
40	(0)		TME	AMGO	TTAN	FOD	SEO	TD	NO:	EE39	7–1						
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			(1)		(A)			GTH:									
					(B)		TYP			eic	Acid						
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			(ii)	ı	KINI (A) (B) (C)	•	SEQU FRAC	JENCI MENT	e or E ASS C TYP CICAL	EMBI	Y MI	IOHT	): ( L Fra					
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			(iv)	1	IMMI (C)	CAIG	CLOI		3:									
••			(v)			TION	_		ME:	With	in I	inv (	Gene	_				
10			(vi)	ı										cons	erved	anti	genic	
						ermin												
			(vii	i)	SEQU	JENCE	E DES	SCRII	MOIT?	i:								
15	SEQ	ID N	10:	EE39	97-1													
	1				5					10					15			
20	Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Arg	Ser	Ile	His	Ile	Gly			
	TGT	ACA	AGĀ	CCC	AAC	AAC	AAT	ACA	AGA	AGA	AGT	ATA	CAC	ATA	GGA			
					20					25					30			
	Pro	G1 v	Arg	Ala		Tvr	A1a	Thr	G1 v		Ile	I1e	G1v	Asn				
25	CCA	GGG	AGA	GCA	TTT	TAT	GCA	ACA	GGA	GAA	ATA	ATA	GGA	AAT	ATA			
					35						:			•				
	Arg	G1n	Ala	Tyr														
30			GCA					•										
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	(2)			RMA					NO: 1									
35			(i)		(V)	UENCI		arac: GTH:	TER I :		<b>5:</b>							
					(B)				Nucle		Acid							
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70			(ii)	)		D (i			e or				n. /	^				
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,					(c)				TICA		1110	· L MA						
			(iii	i)					: HI									
45					(E)		IND	IVID	UAL :	ISOL	ATE:							
			(iv	)		EDIA:			E:									
			()		(C)		CLO		OMP.	W4+1	hin	Ross	Gene					
			(v) (vi)												erved	anti	genic	
50			(VI.	,		ermi			-400		***	F-03			J_ 7 0 U			
			(vi	ii)	SEQ	UENC	E DE	SCRI	PTIO	N:								

SEQ ID NO: EE399-1

1				5					10					15
														G1y
TGT	ACA	AGA	CCC	AAC	AAC	AAT	ACA	AGA	AAA	GGT	ATA	CAT	ATA	GGA

Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asp Ile CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA GAT ATA

Arg Gln Ala His Cys AGA CAA GCA CAT TGT

- INFORMATION FOR SEQ ID NO: EE399-2 (2) SEQUENCE CHARACTERISTICS: (i) LENGTH: 105 (A) TYPE: Nucleic Acid (B) STRANDEDNESS: Single (C) TOPOLOGY: Linear (D) KIND: cDNA to genomic RNA (ii) KIND (if peptide or protein): (ii) (A) SEQUENCE ASSEMBLY METHOD: Overlap FRAGMENT TYPE: Internal Fragment (C) HYPOTHETICAL: (iii) ORIGINAL SOURCE: HIV INDIVIDUAL ISOLATE: (iv) IMMEDIATE SOURCE: CLONE: (C) POSITION IN GENOME: Within Env Gene (v) PROPERTIES OF SEQUENCE: Expresses conserved antigenic (vi) determinant
- SEQ ID NO: EE399-2

(viii)

1 5 10 15
Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His Ile Gly
TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA GGT ATA CAT ATA GGA

SEQUENCE DESCRIPTION:

Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asp Ile CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA GAT ATA 5 Arg Gln Ala His Cys AGA CAA GCA CAT TGT 10 INFORMATION FOR SEQ ID NO: EE399-3 (2) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 TYPE: Nucleic Acid (B) 15 STRANDEDNESS: Single (C) TOPOLOGY: Linear (D) KIND: cDNA to genomic RNA (ii) KIND (if peptide or protein): (ii) SEQUENCE ASSEMBLY METHOD: Overlap (A) FRAGMENT TYPE: Internal Fragment (B) (C) HYPOTHETICAL: (iii) ORIGINAL SOURCE: HIV INDIVIDUAL ISOLATE: (E) (iv) IMMEDIATE SOURCE: 25 CLONE: POSITION IN GENOME: Within Env Gene (v) PROPERTIES OF SEQUENCE: Expresses conserved antigenic (vi) determinant (viii) SEQUENCE DESCRIPTION: 30 SEQ ID NO: EE399-3 35 Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Ser Ile His Ile Gly TGT ACA AGA CCC AAC AAC AAT ACA AGA AGA AGT ATA CAT ATA GGA 40 25 20 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asn Ile CCA GGG AGA GCA TIT TAT ACA ACA GGA GAA ATA ATA GGA AAT ATA 45 Arg Gln Ala His Cys AGA CAA GCA CAT TGT

	(2)		INF	ORMA?					1 : OV								
			(i)		SEQU	JENCI	E CHA	ARAC'	TER IS	STICS	S:						
					(A)		LEN	GTH:	105	5							
					(B)		TYPI	E: 1	Nucle	eic <i>E</i>	lcid						
5					(C)		STR	ANDE	DNES	S: S	Sing	le					
					(D)		TOP	DLOG	Y: ]	Line	ar						
			(ii)	)	KINI	D: cl	DNA 1	to go	enomi	ic Ri	A						
			(ii)	)	KIN	ii) (	E pe	ptido	e or	prot	tein	<b>)</b> :					
					(A)		SEQU	JENCI	E ASS	<b>EMBI</b>	LY MI	ETHO1	): (	)ver]	lap		
10					(B)		FRAC	MEN'	r Tyl	PE:	Inte	erna]	l Fra	agmer	ıt		
					(C)		HYP	THE:	rica:	.: _							
			(ii:	i)	ORIG	GINA	L SOI	JRCE	HIV:	7							
					(E)		IND:	IVIDI	JAL 1	SOL	ATE:						
			(iv	)	IMM	EDIA:	re so	OURC	E:								
15					(C)		CLO							_			
			(v)						OME:								_
			(vi	)				OF S	EQUE	VCE:	Exp	pres	ses o	conse	rved	antig	enic
					dete	ermiı	nant										
20			(vi	ii)	SEQ	JENCI	E DES	SCRI	PTIO	1:							
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	SEQ	ID I	10:	EE40	)5–1												
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	Cys	Inr	Arg	rro	ABII	WRIT	AAT	THE	AGA	TAR	VCV	ATA	ACT	ACC	GCA		
	161	ACA	AGA	CCC	MAC	AAC	WUT	nun	AUA	nnn	non	nin	MOI	noo			
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	Pro	C1 w	Ara	Va1		Tur	Thr	Thr	G1y		Tie	Tle	G1 v	Agp			
	CCC	GCC	VCV	CTA	TAT	TAT	ACA	ACA	GGA	GAA	ATA	ATA	GGA	GAT	ATA		
	CCG	999	non	OILL	1111				-								
35					35												
	Are	Lvs	Ala	His	Cvs												
	_	-		CAT													
40	(2)		INF	ORMA'	TION	FOR	SEQ	ID 1	NO:	BE40!	5–2						
			(i)		SEQ	UENC	E CH	ARAC	TERI	STIC	S:				•		
					(A)		LEN	GTH:	10	5				-			
					(B)		TYP	<b>E:</b> 1	Nucl	eic /	Acid						
					(C)		STR	ANDE	DNES	S: :	Sing	1e					
45					(D)		-	OLOG		Line							
			(ii	)	KIN	D: c	DNA	to g	enom	ic R	NA						

5	(ii)				(A) (B) (C)	O (if	SEQU FRAC HYPO	JENC) MEN' DTHE'	E ASS C TYI CICAI	SEMBI PE: L: _	LY MI	): ETHOI erna!			_		
			(iv)		(E)		IND	(VIDI	JAL 1		ATE:					·	
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			(vi	,		ermin		JF 51	rdom	ACE:	E.X.	bres	ses (	COHS	sivea	antigeni	ت
			(vi	ii)		JENCI		SCRII	TIO	1:							
15	SEQ	ID I	10:	EE40	)5–2												
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	l Cvs	Thr	Arg	Pro		Asn	Asn	Thr	Arg		Arg	Ile	Thr	Thr			
20	TGT	ACA	AGA	CCC	AAC	AAC	AAT	ACA	AGA	AAA	AGA	ATA	ACT	ACG	GGA		
					20					25					30		
25	Pro	G1y	Arg	Val	Tyr	Tyr	Thr	Thr	Gly	Glu	Ile	Ile	Gly	Asp	Ile		
	CCG	GGG	AGA	GTA	TAT	TAT	ACA	AUA	GGA	GAA	WIW	ATW	GGA	GMI	nın		
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30	_	-	GCA		-								•				
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35			(1)		(A)	J11101		GTH:	10		•						
					(B)		TYP	E: 1	Nucle	eic A	Acid						
					(C)				DNES:		Sing	le					
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45			(ii:	i)		G INA					A 1777 .						
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			(v)			ITIO			OME:	Wit	hin	Env (	Gene				
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			(vi	ii)		UENC		SCRI	PTIO	N:							

SEQ ID NO: EE405-3

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10 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Lys Ile Thr Thr Gly TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AAA ATA ACT ACG GGA 20 25 10 Pro Gly Arg Val Tyr Tyr Thr Thr Gly Glu Ile Ile Glu Asp Val CCG GGG AGA GTA TAT TAT ACA ACA GGA GAA ATA ATA GAA GAT GTA 35 15 Arg Lys Ala His Cys AGA AAA GCA CAT TGT INFORMATION FOR SEQ ID NO: EE505-1 (2) 20 SEQUENCE CHARACTERISTICS: (i) (A) LENGTH: 105 TYPE: Nucleic Acid (B) STRANDEDNESS: Single (C) TOPOLOGY: Linear (D) 25 KIND: cDNA to genomic RNA (ii) KIND (if peptide or protein): (ii) SEQUENCE ASSEMBLY METHOD: Overlap (A) (B) FRACMENT TYPE: Internal Fragment HYPOTHETICAL: (C) 30 (iii) ORIGINAL SOURCE: HIV INDIVIDUAL ISOLATE: (E) IMMEDIATE SOURCE: (iv) CLONE: (C) POSITION IN GENOME: Within Env Gene (v) 35 PROPERTIES OF SEQUENCE: Expresses conserved antigenic (vi) determinant (viii) SEQUENCE DESCRIPTION: SEQ ID NO: EE505-1 10 Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Ser Ile Asn Ile Gly

125

TGT ACA AGG CCC AAC AAC AAT ACA AGA AGA AGT ATA AAT ATA GGA

					20					25					30	
	Pro	G1y	Arg	Ala	Phe	Tyr	Ala	Thr	G1y	Asp	Ile	Thr	Gly	Asp	Ile	
	CCA	GGG	AGA	GCA	TTT	TAT	GCA	ACA	<b>GGA</b>	GAT	ATA	ACA	GGA	GAT	ATA	•
	00	•••														
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	Arg	G1n	Ala	His	Cys											
	AGA	CAA	GCA	CAT	TGT											
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	(2)		TNE	ODMAT	TTON	FOR	SEO	ID I	io: F	R50	5-2					
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			(i)		-	)EN(					•					
					(A)			GTH:	105							
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15					(C)		STR	ANDEI	DNESS	S: S	Sing	le				
					(D)		TOP	OLOG	<b>:</b> 1	Linea	ar					
			(ii	)	KIN	D: cl	DNA ·	to ge	enom	ic Ri	A					
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20					(B)			GMEN:								
											Inc	CIMA.		- <b>6</b>		.*
					(C)			OTHE:								
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25					(C)		CLO	NE:						_		
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			(ví											cons	erved	antigenic
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30			(AT	ii)	3EQ	OMAC	בי ע	DONI	110			- A				
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35	1				5					10					15	
	Cvs	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Arg	Ser	Ile	Asn	Ile	G1y	
	TCT	ACA	AGG	CCC	AAC	AAC	AAT	ACA	AGA	AGA	AGT	ATA	AAT	ATA	GGA	
	101	21(41	1100	000												
40										95					20	
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	Pro	G1 y	Arg	Ala	Phe	Tyr	Ala	Thr	Gly	Asp	He	Thr	GLY	Asp	TTE	
	CCA	GGG	AGA	GCA	TTT	TAT	GCA	ACA	GGA	GAT	ATA	ACA	GGA	GAT	ATA	
45					35											
	A	C1-	A1~	m4~	Сув											
	AGA	UAA	GCA	UAT	TGT											

	(2)		INF(	ORMA?	CION	FOR	SEQ	ID I	NO: 1	BE505	5–3					
			(i)		SEQ	JENCI	CHA	ARAC'	rer i	STICS	3:					
					(A)		LEN	GTH:					•			
					(B)		TYP	E: 1	Nucle	eic A	lcid					
5					(C)				DNES		Singl	le				
					(D)					Linea			2			
			(ii)	)	KINI	D: cl	DNA	to g	enom	ic Ri	Αİ		•			
			(ii	)	KINI	) (ii	f pe	ptide	e or	prot	tein)	<b>)</b> :				
					(A)		SEQ	JENC	E AS	SEMBI			): (			
10					(B)		FRA	MEN:	r TY	PB:	Inte	rnal	l Fra	agmer	ıt	
					(C)		HYP	OTHE:	rica:	<b>ւ։</b> _						
			(iii	i)	ORIG	GINA	L SO	URCE	: HI	V						
					(E)		IND	IVID	UAL :	ISOL	ATE:					
			(iv	)	IMM	EDIA'	re s	OURC	E:							
15					(C)		CLO							-		
			(v)		POS:	ITIO	N IN	GEN	OME:	Witl	nin J	inv (	Gene			
			(vi	)				OF S	EQUE	NCE:	Exp	pres	ses (	conse	erved	antigenic
						ermiı										
20			(vi:	ii)	SEQ	UENC	E DE	SCRI	PTIO	N:						
20											•	•				
	SEQ	ID 1	: ON	EE50	)5–3											
25	1				5					10					15	
	Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Arg	Ser	Ile	Asn	Ile	Gly	
	TGT	ACA	AGG	CCC	AAC	AAC	AAT	ACA	AGA	AGA	AGT	ATA	AAT	ATA	GGA	
30													•		20	
30					20	_			<b>01</b>	25	T1 -			A	30	
	Pro	Gly	Arg	Ala	rhe	Tyr	ALA	INT	GIA	ASP	TIE	THE	CCA	CAT	ATA	
	CCA	GGG	AGA	GCA	TTT	IAI	GUA	ACA	GGA	GAI	WIW	AUA	GGA	GAI	um	
35					35											
	A = a	G1n	Δ1a	His												
,				CAT												
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40	(2)			ORMA'												
			(i)			UENC				STIC	S:					
					(A)			GTH:		_						
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			(vi	lí)				SCRII	PTIO	<b>í:</b>						
15	SEQ	ID 1	10:	EE50	)7–1											
	1				5					10					15	
20	Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile	Asn	Ile ATA	G1y CCA	
	161	AUA	AGA	CCC	AAC	AAC	WI	AUA	מטמ	nnn	AGI	NIN	wi	nın	Guz	
					20					25					30	
	Pro	G1y	Arg	Ala	Phe	Tyr	Ala	Thr	G1y	Glu	I1e	Ile	G1y	Asp	Ile	
25	CCA	GGG	AGĀ	GCA	TTT	TAT	GCA	ACA	GGA	GAA	ATA	ATA	GGA	GAT	ATA	
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35			(i)		SEQ!	UENC		arac: GTH:	TER I :		5:					
					(B)		TYP		Nucl		Acid					
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SEQ ID NO: EE509-1 10 5 5 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His Ile Gly TGT ACA AGA CCC AAC AAC AAT ACA AGG AAA GGT ATA CAT ATA GGA 20 25 10 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile CCG GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA 15 Arg Gln Ala His Cys AGA CAA GCA CAT TGT INFORMATION FOR SEQ ID NO: EE509-2 (2) 20 SEQUENCE CHARACTERISTICS: (i) (A) LENGTH: 105 (B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single (D) TOPOLOGY: Linear 25 KIND: cDNA to genomic RNA (ii) (ii) KIND (if peptide or protein): SEQUENCE ASSEMBLY METHOD: Overlap (A) (B) FRAGMENT TYPE: Internal Fragment (C) HYPOTHETICAL: ORIGINAL SOURCE: HIV (iii) INDIVIDUAL ISOLATE: (iv) IMMEDIATE SOURCE: CLONE: (v) POSITION IN GENOME: Within Env Gene 35 PROPERTIES OF SEQUENCE: Expresses conserved antigenic (vi) determinant SEQUENCE DESCRIPTION: (viii) 40 SEQ ID NO: EE509-2

1 5 10 15
Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His Ile Gly
TGT ACA AGA CCC AAC AAC AAT ACA AGG AAA GGT ATA CAT ATA GGA

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					20					25					30		
	Pro	G1y	Arg	Ala	Phe	Tyr	Ala	Thr	G1y	G1u	Ile	Ile	Gly	Asp	Ile		
	CCG	GGG	AGA	GCA	TTT	TAT	GCA	ACA	GGA	GAA	ATA	ATA	GGA	GAT	ATA		
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			(1)		(A)	1574C1	LEN		102		•						
					(B)		TYP		Nucle		Acid						
15					(c)				DNES		Sing	le					
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20					(A)		SEQ	UENC	B AS	SEMBI	LY M	ETHO	): (	)ver	lap		
					(B)		FRA	GMEN.	r TY	PE:	Inte	erna.	l Fra	agmei	ıt		
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			(ii:	i)		GINA			: HIV								
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	Pro	G1 v	Ala	Phe		Thr	Thr	G1v	Asp	Ile	Ile	Gly	Asp	Ile	Arg		
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		Ala		-													
	CAA	GCA	CAT	TGT													
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			(i)		SEQUAL (A)	UENCI		GTH:	TER 19		9:					
_					(B)				Nucle		Acid					
5					(c)				DNESS		Sing	1e				
					(D)			OLOG		Line	-					
			(ii)	)	•	D: cl			enomi	-	-					
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					(c)		HYP	OTHE'	TICA	ւ։						
			(ii:	i)	ORIG	GINA	L SO	URCE	: HIV	7						
					(E)		IND	IVID	UAL 1	ISOL	ATE:					
15			(iv	)	IMM	EDIA:	re s	OURC	E:							
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						ermi										
20			(vi	ii)	SEQ	UENC	E DE:	SCRI	PTIO	N:						
	SEQ	ID I	NO:	EE5	LO-2											
25					5					10					15	
	1	77h	A	D		A	A	Th.	Arg			T16	Hic	Tla		
	TOT	THE	VCV	CCC	ACT	VAU	TAA	ACA	AGA	VCV	CCT	ATA	CAT	ATA	CCT	
	161	nun	nun	CCC	MOI	mo	IMIL	11041			<b>401</b>					
30																
					20					25					30	
	Pro	Gly	Ala	Phe	Tyr	Thr	Thr	G1y	qaA	Ile	Ile	G1y	Asp	Ile	Arg	
	CCA	GGA	GCA	TTT	TAT	ACA	ACA	GGA	GAC	ATA	ATA	GGA	GAT	ATA	AGA	
35					35											
	01-	A1.	TI -	0	33											
			His CAT													
	CAN	GUA	WII	101												
40			•													
	(2)		INF	ORMA:	<b>TION</b>	FOR	SEQ	ID	NO:	ee51	0-3					
			(i)		SEQ	UENC	E CH	ARAC	TERI	STIC	S:					
					(A)			GTH:	10	_						
					(B)				Nucl							
45					(C)				DNES		Sing	le				
					(D)			OLOG		Line						
			(ii	)	KIN	D: c	DNA	to g	enom	ic R	NA					

KIND (if peptide or protein): (ii) SEQUENCE ASSEMBLY METHOD: Overlap (A) FRAGMENT TYPE: Internal Fragment (B) HYPOTHETICAL: (C) 5 ORIGINAL SOURCE: HIV (iii) INDIVIDUAL ISOLATE: (E) IMMEDIATE SOURCE: (iv) CLONE: (C) POSITION IN GENOME: Within Env Gene (v) PROPERTIES OF SEQUENCE: Expresses conserved antigenic 10 (iv) determinant SEQUENCE DESCRIPTION: (viii) 15 SEQ ID NO: EE510-3 10 5 Cys Thr Arg Leu Ser Asn Asn Thr Arg Arg Gly Ile His Ile Gly TGT ACA AGA CTC AGC AAC AAT ACA AGA AGA GGT ATA CAT ATA GGT 20 25 20 Pro Gly Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile Arg CCA GGA GCA TIT TAT ACA ACA GGA GAT ATA ATA GGA GAT ATA AGA 25 ٤, 35 Gln Ala His Cys

CAG GCA CAT TGT

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	(2)	INFORMA	TION FOR SEQ ID NO: EE520-1 SEQUENCE CHARACTERISTICS:
			(A) LENGTH: 105
5			(B) TYPE: Nucleic Acid
•			(C) STRANDEDNESS: Single
		(11)	(D) TOPOLOGY: Linear
		(ii)	KIND: cDNA to genomic RNA
		(ii)	KIND (if peptide or protein):
10			(A) SEQUENCE ASSEMBLY METHOD: Overlap
			(B) FRAGMENT TYPE: Internal Fragment
			(C) HYPOTHETICAL:
		(iii)	ORIGINAL SOURCE: HIV
		(1-)	(E) INDIVIDUAL ISOLATE:
15		(iv)	IMMEDIATE SOURCE:
		()	(C) CLONE:
		(v)	POSITION IN GENOME: Within Env Gene
		(vi)	PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
		(	
20		(viii)	SEQUENCE DESCRIPTION:
	CEO ID	NO: EE5	20_1
	ord in	NO: EES	20-1
25	1		5 10 15
		. Ara Pro	Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly
			AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA
	IGI AGA	A AGA CCC	NAC AND
30			20 25 30
	Pro Clu	Ara Ala	Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile
,			TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA
	Our Coc	, ,,,,,,	
35			35
	Are Gla	Ala His	
		GCA CAT	
,	non ou		
40	(2)	TNFORMA	TION FOR SEQ ID NO: EE520-2
	(-)	(i)	SEQUENCE CHARACTERISTICS:
		(-)	(A) LENGTH: 105
			(B) TYPE: Nucleic Acid
			(C) STRANDEDNESS: Single
45			(D) TOPOLOGY: Linear
		(ii)	KIND: cDNA to genomic RNA
		(ii)	KIND (if peptide or protein):
		(11)	(A) SEQUENCE ASSEMBLY METHOD: Overlap
			(B) FRAGMENT TYPE: Internal Fragment
50			(C) HYPOTHETICAL:
			(0) HII AINDI IONN.

		(iii)	ORIGINAL SOURCE: HIV (E) INDIVIDUAL ISOLATE:
. • •		(iv)	IMMEDIATE SOURCE:
5		(v)	(C) CLONE: POSITION IN GENOME: Within Env Gene
		(vi)	PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
		(viii)	
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	SEQ ID	NO: EE5	20–2
	1		5 10 15
15	Cvs Thr	Arg Pro	Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly
	TGT ACA	AGA CCC	AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA
			20 25 30
20	Pro Clv	Are Ala	Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile
	CCA GGG	AGA GCA	TIT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA
			35
25	Ara Gla	Ala His	
		GCA CAT	
	(2)	TNEODMA	TION FOR SEQ ID NO: EE520-3
30	(2)	(i)	SEQUENCE CHARACTERISTICS:
*		(*/	(A) LENGTH: 105
			(B) TYPE: Nucleic Acid
		•	(C) STRANDEDNESS: Single
oe.			(D) TOPOLOGY: Linear
35		(ii)	KIND: cDNA to genomic RNA
		(ii)	KIND (if peptide or protein):
			(A) SEQUENCE ASSEMBLY METHOD: Overlap (B) FRAGMENT TYPE: Internal Fragment
			(B) FRAGMENT TYPE: Internal Fragment (C) HYPOTHETICAL:
40		(iii)	ORIGINAL SOURCE: HIV
		(111)	(E) INDIVIDUAL ISOLATE:
		(iv)	IMMEDIATE SOURCE:
			(C) CLONE:
		(v)	POSITION IN GENOME: Within Env Gene
45		(vi)	PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
		(viii)	SEQUENCE DESCRIPTION:
	1		•

SEQ ID NO: EE520-3

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5	1 Cys Thr TGT ACA	5 Arg Pro Asn Asn AGA CCC AAC AAC	Asn Thr Arg	10 Lys Ser Ile His AAA AGT ATA CAT	15 Ile Gly ATA GGA
10	Pro Gly CCA GGG	20 Arg Ala Phe Tyr AGA GCA TTT TA	Ala Thr Gly	25 Glu Ile Ile Gly GAA ATA ATA GGA	30 7 Asp Ile A GAT ATA
15	-	35 Ala His Cys GCA CAT TGC			
20	(2)	(A) (B)	CE CHARACTERIS LENGTH: 105 TYPE: Nucle	STICS: Seic Acid	
25		(ii) KIND (: (A) (B)	STRANDEDNESS TOPOLOGY: I CDNA to genomi If peptide or SEQUENCE ASS FRAGMENT TYPE	Linear ic RNA protein): SEMBLY METHOD:	
30		(E)	HYPOTHETICAL AL SOURCE: HIV INDIVIDUAL 1 ATE SOURCE:	1	
35	·	(vi) PROPER		_	
40	SEQ ID 1	NO: EE528-1			
45		5 Arg Pro Asn Asn AGA CCC AAC AA			

5	Pro CCA	Gly GGG	Arg AGA	Ala GCA	20 Val GTT	Tyr TAT	Ala GCA	Thr ACA	Asp GAT	25 Lys AAA	Ile ATA	Ile ATA	Gly GGA	Asn AAT	30 Ile ATA	
10				His CAT												
·	(2)		INF(	RMAT	SEQU (A)		LENG	ARAC'	IO: I TERIS 105	STICS 5	<b>3:</b>					
15			(ii)				STRA TOPO	ANDEI OLOGY	Nucle ONESS 7: I	S: S Lines Lc RM	Singl ur VA					
20			(ii)		(A) (B) (C)		SEQU FRAC HYP(	JENCI MENT OTHE	or S ASS F TYI	SEMBI PE: L:	Y ME	IOHT	): (			
			(111		(E)	INA			: HIV JAL ]		ATE:					
25			(iv) (v) (vi)		(C) Posi	TIO		VE:	ME:		Exp	pres	ses (		erved	
25			(v) (vi)	) Li)	(C) POSI PROI SEQU	TIOI PERT	CLOI N IN IES (	NE: GENO OF SI	ME:	NCE:	Exp	pres	ses (		erved minant	
	SEQ	ID 1	(v) (vi)	)	(C) POSI PROI SEQU	TIOI PERT	CLOI N IN IES (	NE: GENO OF SI	OME:	NCE:	Exp	pres	ses (			
	1 Cys	Thr	(v) (vi) (vi)	ii) EE52 Pro	(C) POSI PROI SEQU 28-2	TION PERT: JENCI	CLOI N IN IES ( E DE:	VE: GENO OF SI SCRII	OME:	NCE: N: 10 Arg	Exp ant	ress iger	ses (	lete:	minant 15 Gly	
30	1 Cys TGT	Thr ACA	(vi) (vi) (vi) NO: Arg AGA	Pro CCC	(C) POSI PROI SEQU 28-2 5 Asn AAC 20 Val	ITION PERT: JENCI Asn AAC	CLON IN IN IES (CE DES	VE: GEN( OF SI SCRII Thr ACG	ME: EQUE PTION	NCE: 10 Arg AGA 25 Lys	Gly GGT	Ile ATA	His CAT	Ile ATA	15 Gly GGA 30 Ile	

5	(2)	(i) (ii) (ii)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 105  (B) TYPE: Nucleic Acid  (C) STRANDEDNESS: Single  (D) TOPOLOGY: Linear  KIND: cDNA to genomic RNA  KIND (if peptide or protein):  (A) SEQUENCE ASSEMBLY METHOD: Overlap  (B) FRAGMENT TYPE: Internal Fragment  (C) HYPOTHETICAL:  ORIGINAL SOURCE: HIV  (E) INDIVIDUAL ISOLATE:
15		(iv) (v) (vi)	IMMEDIATE SOURCE:  (C) CLONE:  POSITION IN GENOME: Within Env Gene PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
20	SEQ ID I		•
25	1 Cys Thr TGT ACA	Arg Pro AGA CCC	5 10 15 Asn Asn Asn Thr Arg Arg Gly Ile His Ile Gly AAC AAC AAT ACG AGG AGA GGT ATA CAT ATA GGA
30	Pro Gly CCA GGG	Arg Ala AGA GCA	20 25 30 Val Tyr Ala Thr Asp Lys Ile Ile Gly Asn Ile GTT TAT GCA ACA GAT AAA ATA ATA GGA AAT ATA
35		Ala His GCA CAT	
40	(2)	INFORMAT	TION FOR SEQ ID NO: EE529-1 SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 (B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single (D) TOPOLOGY: Linear
45		(ii) (ii)	KIND: cDNA to genomic RNA KIND (if peptide or protein): (A) SEQUENCE ASSEMBLY METHOD: Overlap (B) FRAGMENT TYPE: Internal Fragment (C) HYPOTHETICAL:
50			

		iii)	ORIGINAL SOURCE: HIV (E) INDIVIDUAL ISOLATE:
	()	iv)	IMMEDIATE SOURCE: (C) CLONE:
5	-	r) ri)	POSITION IN GENOME: Within Env Gene PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
	(7	viii)	SEQUENCE DESCRIPTION:
10	SEQ ID NO	: EE52	29–1
	1		5 10 15
15	Cys Thr A		Ser Asn Asn Thr Arg Arg Ser Ile Pro Ile Gly
	TGT ACA AC	JA CCC	AGC AAC AAT ACA AGA AGT ATA CCT ATA GGA
			20 25 30
20	Pro Gly A	rg Ala	Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile
20	CCA GGG AC	GA GCA	TIT TAT ACA ACA GGA GAT ATA ATA GGA GAT ATA
			25
	Arg Glu Al	la His	35 Cvs
25	AGA CAA GO		
9,	(2) II	VEORMAT	TION FOR SEQ ID NO: EE529-2
		i)	SEQUENCE CHARACTERISTICS:
30			(A) LENGTH: 105 (B) TYPE: Nucleic Acid
			(C) STRANDEDNESS: Single
	C:	ii)	(D) TOPOLOGY: Linear KIND: cDNA to genomic RNA
35		ii)	KIND (if peptide or protein):
			(A) SEQUENCE ASSEMBLY METHOD: Overlap (B) FRAGMENT TYPE: Internal Fragment
			(C) HYPOTHETICAL:
40	(:	iii)	ORIGINAL SOURCE: HIV
	(:	iv)	(E) INDIVIDUAL ISOLATE: IMMEDIATE SOURCE:
			(C) CLONE:
		v) vi)	POSITION IN GENOME: Within Env Gene PROPERTIES OF SEQUENCE: Expresses conserved
45	· ·	<b>*</b>	antigenic determinant
	(-	viii)	SEQUENCE DESCRIPTION:
	•		
50	SEQ ID NO	EE5	29–2

	1				5					10					15
	Cvs	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile	Thr	Ile	Gly
	TGT	ACA	AGA	CCT	AAC	AAT	AAT	ACA	AGA	AAA	AGT	ATA	ACT	ATA	GGA
5															
					20	_				, 25			<b>01</b>	,	30
	Pro	G1y	Arg	Ala	Phe	Tyr	Ala	Thr	Gly	Asp	TTE	Ile	GIA	ASP	116
	CCG	GGG	AGA	GCA	TTT	TAT	GCA	AUA	GGA	GAU	AIA	ATA	GGA	GAI	VIV
10											•				•
					35										
	Ara	Cln	A1a	His											
				CAT											
	11011	<b></b>	00												
15															
	(2)		INF	ORMA'	CION	FOR	SEQ	ID I	1:08	EE53	3–1				
			(i)			JENCI			TER I		S:				
					(A)				10			•			
00					(B)		TYPI		Nucle						
20					(C)				r: ]		Sing	re		•	
			(11		(D)	اء ما			enom:					٠.	
			(ii)		KIMI	1 (4)	י מאנע די מאנע	ntid	enom.	nroi	tein	):			
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					(B)				r TY			erna			
25					(D)									~D~~	
25									TICA						
25			( <b>ii</b> :	i)	(C)	SINA:	HYP	)THE		L: .					
25			( <b>ii</b> :	i)	(C)	GINA:	HYP L SO	othe URCE	TICA:	L: V					
,			(ii:	)	(C) ORIG (E) IMM		HYPO L SO IND TE SO	OTHE URCE IVID OURC	TICA: : HI UAL	L: V					
25 30			(iv	)	(C) ORIG	EDIA'	HYPO L SOU IND TE SO CLOI	OTHE URCE IVID OURC NE:	TICA: HIV UAL E:	L: V ISOL	ATE:	-			
,			(iv (v)	)	(C) ORIG (E) IMMI (C) POS	EDIA'	HYPO L SOU IND: TE SO CLOI N IN	OTHE URCE IVID OURC NE: GEN	TICA: HIV UAL E: OME:	L: V ISOL	ATE:	Env (	Gene		
,			(iv	)	(C) ORIG (E) IMMI (C) POS	EDIA'	HYPO L SOU IND: TE SO CLOI N IN	OTHE URCE IVID OURC NE: GEN	TICA: HIV UAL E: OME:	L: V ISOL	ATE:	Env (	Gene	cons	erved
,			(iv (v) (vi	)	(C) ORIC (E) IMMI (C) POS: PROI	EDIA ETIO PERT	HYPO L SOU IND TE SO CLOU N IN IES	OTHE URCE IVID OURC NE: GEN	TICA: HI' UAL E: OME: EQUE	L: V ISOL Wit	ATE:	Env (	Gene	cons	
,			(iv (v) (vi	)	(C) ORIC (E) IMMI (C) POS: PROI	EDIA ETIO PERT	HYPO L SOU IND TE SO CLOU N IN IES	OTHE URCE IVID OURC NE: GEN	TICA: HI' UAL E: OME: EQUE	L: V ISOL Wit	ATE:	Env (	Gene	cons	erved
<b>30</b>			(iv (v) (vi	)	(C) ORIC (E) IMMI (C) POS: PROI	EDIA ETIO PERT	HYPO L SOU IND TE SO CLOU N IN IES	OTHE URCE IVID OURC NE: GEN	TICA: HI' UAL E: OME: EQUE	L: V ISOL Wit	ATE:	Env (	Gene	cons	erved
<b>30</b>	SEO	ID 1	(iv (v) (vi (vi	) ii)	(C) ORIC (E) IMMI (C) POS: PRO!	EDIA' ETIO PERT UENC	HYPO L SOU IND TE SO CLOU N IN IES	OTHE URCE IVID OURC NE: GEN	TICA: HI' UAL E: OME: EQUE	L: V ISOL Wit	ATE:	Env (	Gene	cons	erved
<b>30</b>	SEQ	<b>ID</b> 1	(iv (v) (vi (vi	)	(C) ORIC (E) IMMI (C) POS: PRO!	EDIA' ETIO PERT UENC	HYPO L SOU IND TE SO CLOU N IN IES	OTHE URCE IVID OURC NE: GEN	IICA: HI' UAL E: OME: EQUE	L: V ISOL Wit	ATE:	Env (	Gene	cons	erved
<b>30</b>	SEQ	<b>ID</b> 1	(iv (v) (vi (vi	) ii)	(C) ORIC (E) IMMI (C) POS: PRO!	EDIA' ETIO PERT UENC	HYPO L SOU IND TE SO CLOU N IN IES	OTHE URCE IVID OURC NE: GEN	IICA: HI' UAL E: OME: EQUE	L: V ISOL Wit	ATE:	Env (	Gene	cons	erved rminant
<b>30</b>	1		(iv (v) (vi (vi:	) ii) EE5	(C) ORIG (E) IMMI (C) POS: PROI SEQI	EDIA ETIO PERT	HYPOL SOLUTION IN IN INC.	OTHE URCE IVID OURC NE: GEN OF S	TICA: HIVUAL E: OME: EQUE	L: V ISOL Wit NCE:	hin Ex an	Env (pres	Gene ses nic	- cons dete	erved rminant
30 35	1 Cys	Thr	(iv (v) (vi (vi:	) ii) EE5	(C) ORIG (E) IMMI (C) POS: PROI SEQ! 33-1	EDIA ITIO PERT UENC	HYPOL SOU IND IE SO CLOI N IN IES O	OTHE URCE IVID OURC: GEN OF S SCRI	TICA: HIVUAL E: OME: EQUE PTIO	L: V ISOL Wit NCE: N:	hin Ex an	Env prestige	Gene ses nic	cons	erved rminant
30 35	1 Cys	Thr	(iv (v) (vi (vi:	) ii) EE5	(C) ORIG (E) IMMI (C) POS: PROI SEQ! 33-1	EDIA ITIO PERT UENC	HYPOL SOU IND IE SO CLOI N IN IES O	OTHE URCE IVID OURC: GEN OF S SCRI	TICA: HIVUAL E: OME: EQUE PTIO	L: V ISOL Wit NCE: N:	hin Ex an	Env prestige	Gene ses nic	cons	erved rminant
30 35	1 Cys	Thr	(iv (v) (vi (vi:	) ii) EE5	(C) ORIG (E) IMMI (C) POS: PROI SEQ! 33-1	EDIA ITIO PERT UENC	HYPOL SOU IND IE SO CLOI N IN IES O	OTHE URCE IVID OURC: GEN OF S SCRI	TICA: HIVUAL E: OME: EQUE PTIO	L: V ISOL Wit NCE: N:	hin Ex an	Env prestige	Gene ses nic	cons	erved rminant
35 ,	1 Cys	Thr	(iv (v) (vi (vi:	) ii) EE5	(C) ORIC (E) IMMI (C) POS: PROI SEQ! 33-1	EDIA ITIO PERT UENC	HYPOL SOU IND IE SO CLOI N IN IES O	OTHE URCE IVID OURC: GEN OF S SCRI	TICA: HIVUAL E: OME: EQUE PTIO	L: V ISOL Wit NCE: N:	hin Ex an	Env prestige	Gene ses nic	cons	erved rminant 15 Gly GGA
30 35	1 Cys TGT	Thr ACA	(iv (v) (vi (vi: NO:	) ii) EE5 Pro	(C) ORIC (E) IMMI (C) POS: PROI SEQI 33-1	EDIA TTIO: PERT UENC	HYPOL SOLUTION IN IN IES CASTA	OTHE URCE IVIDOURCE NE: GEN DF S SCRI	rica: HIV UAL E: OME: EQUE PTIO	L: V ISOL Wit NCE: N:	hin Ex an Ser AGT	Env pres tige	Gene ses nic Pro	cons dete	erved rminant 15 Gly GGA
35 ,	1 Cys TGT	Thr ACA	(iv (v) (vi (vi: NO: Arg AGA	) ii) EE5 Pro CCC	(C) ORIC (E) IMMI (C) POS: PROI SEQ! 33-1 5 Asn AAC 20 Phe	EDIA TITIO PERT Asn AAC	HYPOL SOLUTION IN IN IES OF ASTRONOMY ASTRONOM	OTHE URCE IVIDOURCE NE: GEN OF S SCRI	rica: Hive UAL E: OME: EQUE PTIO	L: V ISOL Wit NCE: N:	hin Ex an Ser AGT	Env prestige	Gene ses nic	cons dete Ile ATA	erved rminant 15 Gly GGA

Arg Gln Ala His Cys AGA CAA GCA CAT TGT (2) INFORMATION FOR SEQ ID NO: EE533-2 SEQUENCE CHARACTERISTICS: (i) LENGTH: 105 (A) (B) TYPE: Nucleic Acid 10 STRANDEDNESS: Single (C) TOPOLOGY: Linear (D) KIND: cDNA to genomic RNA (ii) KIND (if peptide or protein): (ii) SEQUENCE ASSEMBLY METHOD: Overlap (A) 15 FRAGMENT TYPE: Internal Fragment (B) (C) HYPOTHETICAL: (iii) ORIGINAL SOURCE: HIV INDIVIDUAL ISOLATE: (iv) IMMEDIATE SOURCE: 20 CLONE: POSITION IN GENOME: Within Env Gene (v) PROPERTIES OF SEQUENCE: Expresses conserved (vi) antigenic determinant SEQUENCE DESCRIPTION: (viii) 25 SEQ ID NO: EE533-2 30 10 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Pro Ile Gly TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CCT ATA GGA 30 20 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile CCA GGG AGA GCA TTT TAT ACA ACA GGA GAT ATA ATA GGA GAT ATA Arg Gln Ala His Cys AGA CAA GCA CAT TGT (2) INFORMATION FOR SEQ ID NO: EE533-3 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 (B) TYPE: Nucleic Acid STRANDEDNESS: Single (C)

		(ii) (ii)	(D) TOPOLOGY: Linear KIND: cDNA to genomic RNA KIND (if peptide or protein):
		(11)	(A) SEQUENCE ASSEMBLY METHOD: Overlap
5			(B) FRACMENT TYPE: Internal Fragment
			(C) HYPOTHETICAL:
		(iii)	ORIGINAL SOURCE: HIV (E) INDIVIDUAL ISOLATE:
		(iv)	IMMEDIATE SOURCE:
10			(C) CLONE:
		(v)	POSITION IN GENOME: Within Env Gene
		(vi)	PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
15		(viii)	SEQUENCE DESCRIPTION:
	SEQ ID	NO: EE5	33–3
00	1		5 10 15
20	Cys Thr	Arg Pro	Asn Asn Asn Thr Arg Lys Ser Ile Pro Ile Gly
	TGT ACA	AGA CCC	AAC AAC AAT ACA AGA AAA AGT ATA CCT ATA GGA
			20 25 30
25	Pro Gly	Arg Ala	Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile
	CCA GGG	AGA GCA	TTT TAT ACA ACA GGA GAT ATA ATA GGA GAT ATA
	•		35
30	Arg Gln	Ala His	Cys
	AGA CAA	GCA CAT	TGT
	(2)	INFORMA	TION FOR SEQ ID NO: EE535-1
35		(i)	SEQUENCE CHARACTERISTICS:
			(A) LENGTH: 105
			(B) TYPE: Nucleic Acid
			(C) STRANDEDNESS: Single
40			(D) TOPOLOGY: Linear
40		(ii)	KIND: cDNA to genomic RNA
		(ii)	KIND (if peptide or protein):
			(A) SEQUENCE ASSEMBLY METHOD: Overlap
			(B) FRAGMENT TYPE: Internal Fragment
45			(C) HYPOTHETICAL:
		(iii)	ORIGINAL SOURCE: HIV
			(E) INDIVIDUAL ISOLATE:
		(iv)	IMMEDIATE SOURCE:
		(·)	(C) CLONE:
50		(v) .	POSITION IN GENOME: Within Env Gene

			(vi)	)	PROF	PERT	ies (	)F SI	<b>SQUE</b>	MCE:		•			erved minant	-
			(vii	i)	SEQU	JENCI	E DES	SCRII	PTION	<b>1:</b>	an	rıRei	110	ie ce i	. III III C	•
5																
÷	SEQ	ID 1	10:	EE53	35–1											
10	1				5					10					15	
10	Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile	His	Ile	Gly	
	TGT	ACA	AGA	ccc	AAC	AAC	AAT	ACA	AGA	AAA	AGI	ATA	GAI	ATA	GGA	
					20					25					30	
15	Pro	G1y	Arg	Ala	Phe	Tyr	Ala	Thr	Gly	G1u	Ile	Ile	G1y	Asp	Ile	
	CCA	GGG	AGA	GCA	TTT	TAT	GCA	ACA	GGA	GAA	ATA	ATA	GGA	GAT	ATA	
					35											
20			Ala													
	AGA	CAA	GCA	CAT	TGT											
	(2)		INFO	ORMA:	CION	FOR	SEQ	ID I	NO: 1	EE53:	5–2					
25			(i)		•		E CH				S:					
					(A) (B)				10! Nucle		h-i-A					
					(C)				DNES		Sing	le				
					(D)			DLOG.		Line	_					
30			(ii)	)			DNA									
			(ii)	)			f pe									
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					(B)				TICA:		me	erna	I FI	RRme	uc	
35			(ii:	i)		GINA	L SO			-		<del></del>				
			\	-,	(E)				UAL		ATE:					
			(iv	)	IMM	EDIA'	TE S	OURC	B:							
					(C)		CTO							_		
40			(v)										Gene			
			(vi	)	PRO.	PERT	IES	of S	RÓOE	NCE:		_			erved rminan	
			(vi	ii)	SEQ	UENC	E DE	SCRI	PTIO	N:	an	rike	nic	ue ce	rmindm	
	•															
45	SEQ	ID ?	NO:	EE5	35–2											
	1				5					10					15	
		Thr	Arg	Pro		Asn	Asn	Thr	Arg			Ile	His	Ile	Gly	
50														ATA		

					20					25					30
	Pro	G1y	Arg	Ala	Phe	Tyr	Ala	Thr	G1y	Glu	Ile	Ile	Gly	Asp	Ile
	CCA	GGG	AGA	GCA	TTT	TAT	GCA	ACA	GGA	GAA	ATA	ATA	GGA	GAT	ATA
5															
					35										
	Arg	G1n	Ala	His	Сув										
	AGA	CAA	GCA	CAT	TGT										
10															
	(2)		INF	ORMA'	TION	FOR	SEQ	ID 1	NO: 1	BE543	3-1				
			(i)		SEQ	JENC	E CHA	ARAC'	CER IS	STICS	S:				
					(A)		LEN(	ETH:	10	5 .					
					(B)		TYPI		Nucle		Acid				
15					(C)				DNESS	S: S	Sing	le			
					(D)			)LOG		Linea					
			(ii)				DNA 1								
			(ii)	)			f pe								
					(A)		-						D: (		
20									r Tyl		Inte	erna.	l Fra	agmer	ıt
					(C)				ricai	_					<del></del>
			(ii:	i)		GINA.	L SOI								
					(E)				JAL :	LSOL	ATE:				
25			(iv	)		RDTA:	TE SO		5:						
25			<b>(</b> )		(C)	TOTAL	CLO			1.7.3 4.1	3- 1	2	2	-	
			(v)				N IN								
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	CEU	tn i	<b>ن</b> م	225	43–1										
	Juq	10 1		UUJ.	7 <b>3</b> - 1										
35	1				5					10					15
	_	Thr	Arg	Pro		Asn	Asn	Thr	Arg	Arg	G1v	Ile	Ser	Ile	G1y
							AAT								
40					20					25				_	30
	Pro	G1y	Arg	Ala	Phe	Val	Tyr	Ala	Thr	Lys	Ile	I1e	G1y	Asp	Ile
							TAT								
			•			•									
45					35										
•				His											
	AGA	CAA	GCA	CAT	TGT	•									

5	(2) INFORMA (i)	TION FOR SEQ ID NO: EE543-2 SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 (B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single
	(ii) (ii)	(D) TOPOLOGY: Linear KIND: cDNA to genomic RNA KIND (if peptide or protein): (A) SEQUENCE ASSEMBLY METHOD: Overlap
10	(iii)	(B) FRAGMENT TYPE: Internal Fragment (C) HYPOTHETICAL: ORIGINAL SOURCE: HIV (E) INDIVIDUAL ISOLATE:
15	(iv) (v)	IMMEDIATE SOURCE: (C) CLONE: POSITION IN GENOME: Within Env Gene
	(vi) (viii)	PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
20	SEQ ID NO: EE5	
25	•	
	Cys Thr Arg Pro TGT ACA AGA CCC	5 10 15 Asn Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly AAT AAC AAT ACA AGA AAA AGT ATA ACT ATA GGA
<b>30</b>	Pro Gly Arg Ale	20 25 30 Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile
	CCA GGG AGA GCA	TIT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA
35	Arg Gln Ala His	35 C <b>vs</b>
	AGA CAA GCA CAT	
40	(2) INFORMA	TION FOR SEQ ID NO: EE543-3 SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 (B) TYPE: Nucleic Acid
45	(ii) (ii)	(C) STRANDEDNESS: Single (D) TOPOLOGY: Linear KIND: cDNA to genomic RNA KIND (if peptide or protein):
50		(A) SEQUENCE ASSEMBLY METHOD: Overlap (B) FRAGMENT TYPE: Internal Fragment

					(C)	HYP	OTHE	TICAI	ւ։ .						
			(iii	i)	ORIGINA	L SO	URCE	: HIV	7						
			•		(E)	IND	IVID	UAL 1	ISOL	ATE:					<u>.                                    </u>
			(iv)	)	IMMEDIA	TE S	OURC	E:							
5					(c)	CLO	NE:								
			(v)		POSITIO	N IN	GEN	OME:	Witl	hin	Env	Gene			
			(vi)		PROPER'									erved	l
			•					•			- tige	nic	dete	rmina	int
			(vii	ii)	SEQUENC	E DE	SCRI	PTIO	V:		_		•	•	•
10			•	•	•										
	SE0	ID I	NO:	EE54	3-3										
	•														
15	1				5				10					15	
	Cys	Thr	Arg	Pro	Asn Ası	ı Asn	Thr	Arg	Lys	Ser	Ile	Thr	Ile	Gly	
	TGT	ACA	AGA	CCC	AAT AAG	C AAT	ACA	AGA	AAA	AGT	ATA	ACT	ATA	GGA	
20					20				25		:			30	
	Pro	G1y	Arg	Ala	Phe Ty	: Ala	Thr	G1y	G1u	Ile	Ile	G1y	qaA	Ile	
	CCA	GGG	AGA	GCA	TTT TA	C GCA	ACA	GGA	GAA	ATA	ATA	GGA	GAT	ATA	
															•
25					35										
	Arg	G1n	Ala	His	Cys										
	AGA	CAA	GCA	CAT	TGT										
30															
30	(2)			ORMA:	ION FO	-									
			(i)		SEQUEN					5:					
					(A)		GTH:								
					(B)		E:								
35					(C)		ANDE			Sing	Te				
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			(ii		KIND: (						١.				
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40					(c)		OTHE		_	1110	cıua		agme:		
			( <b>ii</b> :	: \	ORIGIN										
			(11.	ı,	(E)		IVID			<b>ΔΤΓ</b> •					
			(iv	`	IMMEDIA				1901	are.					
			(14	,	(C)		NE:								
45			(v)		POSITION			OMF •	Mi+	hin	Env	Cone			
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			( A T	,	T WOL EW	CHIL	AT D	-40m						rmina	
			(274)	ii)	SEQUEN	er de	SCRT	PTTO	N:	CILI.	Be				
			( • 1.	,	22427										

SEQ ID NO: EE558-1 10 1 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA 20 25 10 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile CCA GGG AGA GCA TIT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA 35 15 Arg Gln Ala His Cys AGA CAA GCA CAT TGC (2) INFORMATION FOR SEQ ID NO: EE558-2 (i) SEQUENCE CHARACTERISTICS: LENGTH: 105 (A) TYPE: Nucleic Acid (B) STRANDEDNESS: Single (C) TOPOLOGY: Linear (D) 25 KIND: cDNA to genomic RNA (ii) KIND (if peptide or protein): (ii) SEQUENCE ASSEMBLY METHOD: Overlap (A) FRAGMENT TYPE: Internal Fragment (B) (C) HYPOTHETICAL: ORIGINAL SOURCE: HIV (iii) INDIVIDUAL ISOLATE: (E) IMMEDIATE SOURCE: (iv) CLONE: (C) POSITION IN GENOME: Within Env Gene (v) PROPERTIES OF SEQUENCE: Expresses conserved (iv) antigenic determinant (viii) SEQUENCE DESCRIPTION: SEQ ID NO: EE558-2

1 5 10 15 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Leu Gly TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT CTA GGG

45

20 25 30 Pro Gly Arg Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile CCA GGG AGA GCA TTT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA

					35											
	Arg	G1n	Ala	His												
				CAT												
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	(2)		INF	ORMA'												
			(i)		•	JENC!	E CHA	ARAC'	CER IS	STICS	S:					
					(A)		LEN(		105							
					(B)				Nucle		Acid					
10					(C)				)NES		Sing	le				
					(D)				<b>?:</b> 1							
			(ii)				DNA 1									
			(ii)	)		) (i	f pej									
					(A)								): (			
15					(B)						Inte	ernal	Fra	igmer	it	
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			( <b>ii</b> :	i)		GINA	L SO									
				-	(E)				JAL 3	CSOL	ATE:					
••			(iv	)		ZDIA'	re so		3:							
20					(C)		CLO							_		
			(v)				NI N									
			(vi	)	PROI	PERT.	es (	OF SI	<b>z</b> Ón <b>E</b> i	MCE:					erved	
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25			(V1:	ii)	SEQ	JENC	E DES	SCRI	STIO	<b>v:</b>						
20																
	CRO	TD 1	٠.	PPS	.0.2											
	SEQ	ID I	10:	EE5	58-3											
	SEQ	ID I	10:	EE5	58-3											
30	,	ID I	10:	EE5						10					15	
30	. 1				5	Asn	Asn	Thr	Arg	10 Lvs	Ser	Ile	His	Leu		
30	l Cys	Thr	Arg	Pro	5 Asn					Lys					Gly	
30	l Cys	Thr	Arg		5 Asn					Lys					Gly	
30	l Cys	Thr	Arg	Pro	5 Asn					Lys					Gly	
30 35	l Cys	Thr	Arg	Pro	5 Asn					Lys					Gly	
	1 Cys TGT	Thr ACA	Arg AGA	Pro CCC	5 Asn AAC	AAC	AAT	ACA	AGA	Lys AAA 25	AGT	ATA	CAT	CTA	G1y GGG	
	1 Cys TGT	Thr ACA	Arg AGA	Pro	5 Asn AAC 20 Phe	AAC	AAT	ACA	AGA Gly	Lys AAA 25 Asp	AGT Ile	ATA	CAT Gly	CTA	Gly GGG 30 Ile	
	1 Cys TGT	Thr ACA	Arg AGA	Pro CCC	5 Asn AAC 20 Phe	AAC	AAT	ACA	AGA Gly	Lys AAA 25 Asp	AGT Ile	ATA	CAT Gly	CTA	Gly GGG 30 Ile	
	1 Cys TGT	Thr ACA	Arg AGA	Pro CCC	5 Asn AAC 20 Phe	AAC	AAT	ACA	AGA Gly	Lys AAA 25 Asp	AGT Ile	ATA	CAT Gly	CTA	Gly GGG 30 Ile	
	1 Cys TGT	Thr ACA	Arg AGA	Pro CCC	5 Asn AAC 20 Phe	AAC	AAT	ACA	AGA Gly	Lys AAA 25 Asp	AGT Ile	ATA	CAT Gly	CTA	Gly GGG 30 Ile	
35	1 Cys TGT Pro	Thr ACA Gly GGG	Arg AGA Arg AGA	Pro CCC	5 Asn AAC 20 Phe TTT	AAC	AAT	ACA	AGA Gly	Lys AAA 25 Asp	AGT Ile	ATA	CAT Gly	CTA	Gly GGG 30 Ile	
35	1 Cys TGT Pro CCA	Thr ACA Gly GGG	Arg AGA Arg AGA	Pro CCC Ala GCA	5 Asn AAC 20 Phe TTT 35 Cys	AAC	AAT	ACA	AGA Gly	Lys AAA 25 Asp	AGT Ile	ATA	CAT Gly	CTA	Gly GGG 30 Ile	
35	1 Cys TGT Pro CCA	Thr ACA Gly GGG	Arg AGA Arg AGA	Pro CCC Ala GCA	5 Asn AAC 20 Phe TTT 35 Cys	AAC	AAT	ACA	AGA Gly	Lys AAA 25 Asp	AGT Ile	ATA	CAT Gly	CTA	Gly GGG 30 Ile	
35	1 Cys TGT Pro CCA	Thr ACA Gly GGG	Arg AGA Arg AGA	Pro CCC Ala GCA	5 Asn AAC 20 Phe TTT 35 Cys	AAC	AAT	ACA	AGA Gly	Lys AAA 25 Asp	AGT Ile	ATA	CAT Gly	CTA	Gly GGG 30 Ile	
35	1 Cys TGT Pro CCA	Thr ACA Gly GGG	Arg AGA Arg AGA	Pro CCC Ala GCA	5 Asn AAC 20 Phe TTT 35 Cys TGT	Tyr TAT	Thr	Thr ACA	Gly GGA	Lys AAA 25 Asp GAC	Ile ATA	ATA	CAT Gly	CTA	Gly GGG 30 Ile	
<b>35</b>	1 Cys TGT Pro CCA	Thr ACA Gly GGG	Arg AGA Arg AGA	Pro CCC Ala GCA His CAT	5 Asn AAC 20 Phe TTT 35 Cys TGT	Tyr TAT	Thr ACA	Thr ACA	Gly GGA	Lys AAA 25 Asp GAC	Ile ATA	ATA	CAT Gly	CTA	Gly GGG 30 Ile	
<b>35</b>	1 Cys TGT Pro CCA	Thr ACA Gly GGG	Arg AGA Arg AGA Ala GCA	Pro CCC Ala GCA His CAT	5 Asn AAC 20 Phe TTT 35 Cys TGT	Tyr TAT	Thr ACA SEQ	Thr ACA	Gly GGA	Lys AAA 25 Asp GAC	Ile ATA	Ile ATA	CAT Gly	CTA	Gly GGG 30 Ile	

5

		(C) STRANDEDNESS: Single
		(D) TOPOLOGY: Linear
	• •	KIND: cDNA to genomic RNA
	(ii)	KIND (if peptide or protein):
1		(A) SEQUENCE ASSEMBLY METHOD: Overlap
		(B) FRAGMENT TYPE: Internal Fragment
		(C) HYPOTHETICAL:
	(iii)	ORIGINAL SOURCE: HIV
	(2	(E) INDIVIDUAL ISOLATE:
0	(iv)	IMMEDIATE SOURCE:
	(20)	(C) CLONE:
	()	POSITION IN GENOME: Within Env Gene
	(v)	PROPERTIES OF SEQUENCE: Expresses conserved
	(iv)	antigenic determinant
5		
•	(viii)	SEQUENCE DESCRIPTION:
	SEQ ID NO: EE59	94–1
20		. 10 15
	1	
	Cvs Thr Arg Pro	Asn Asn Asn Thr MET Lys Ser Ile His Ile Gly
	TGT ACA AGA CCC	AAC AAC AAT ACA ATG AAA AGT ATA CAT ATA GGA
	101 1101 0111	
25		
		20 25 30
	D 01- Ama A1a	Dhe Tur Thr Thr Gly Gln Ile Ile Gly Asp Ile
	Pro Gly Arg Ara	TIT TAT ACA ACA GGA CAA ATA ATA GGA GAT ATA
	CUA GGG AGA GCA	TII IMI MAI MAI ONL
30		
00		OF.
		35
	Arg Gln Ala His	Cys
	AGA CAA GCA CAT	TGT
35		
	(2) INFORMA	TION FOR SEQ ID NO: EE594-2
	(i)	SEQUENCE CHARACTERISTICS:
	<b>\-</b> /	(A) LENGTH: 105
		(B) TYPE: Nucleic Acid
40		(C) STRANDEDNESS: Single
		(D) TOPOLOGY: Linear
	(12)	KIND: cDNA to genomic RNA
	(ii)	KIND (if peptide or protein):
	(ii)	
45		
45		(2)
	•	(C) HYPOTHETICAL:
	(iii)	ORIGINAL SOURCE: HIV
		(E) INDIVIDUAL ISOLATE:
	(iv)	IMMEDIATE SOURCE:
	·- ·	

	(v) (vi)	(C) CLONE:  POSITION IN GENOME: Within Env Gene PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
5	(viii)	
	SEQ ID NO: EE	2594–2
10		
	1	5 10 15
	Cys Thr Arg Pr	o Asn Asn Asn Thr MET Lys Ser Ile His Ile Gly
	TGT ACA AGA CO	CC AAC AAC AAT ACA ATG AAA AGT ATA CAT ATA GGA
15		
		20 25 30
	Pro Gly Are Al	a Phe Tyr Thr Thr Gly Gln Ile Ile Gly Asp Ile
	CCA GGG AGA GC	CA TIT TAT ACA ACA GGA CAA ATA ATA GGA GAT ATA
20		
		35
	Arg Gln Ala Hi	
	AGA CAA GCA CA	IT IGI
25		
	(2) INFORM	MATION FOR SEQ ID NO: EE594-3
	(i)	SEQUENCE CHARACTERISTICS:
	,	(A) LENGTH: 105
30		(B) TYPE: Nucleic Acid
30		(C) STRANDEDNESS: Single
	(11)	(D) TOPOLOGY: Linear KIND: cDNA to genomic RNA
	(ii) (ii)	KIND (if peptide or protein):
	(11)	(A) SEQUENCE ASSEMBLY METHOD: Overlap
35	•	(B) FRACMENT TYPE: Internal Fragment
		(C) HYPOTHETICAL:
	(iii)	
		(E) INDIVIDUAL ISOLATE:
40	(iv)	IMMEDIATE SOURCE:
	()	(C) CLONE: POSITION IN GENOME: Within Env Gene
	(v) (vi)	PROPERTIES OF SEQUENCE: Expresses conserved
	(41)	antigenic determinant
	(viii	
45	•	·       •
	SEQ ID NO: E	E594~3

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	1				5						G	T1.	п1 -	†1a		
	Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	WEI	Lys	Ser	116	DIP	TTC	CCA	
	TGT	ACA	AGA	CCC	AAC	AAC	AAT	ACA	ATG	AAA	AGI	ATA	CAI	HIM	GGA	
5																
3															30	
					20					25			<b>~1</b>	<b>A</b>		
	Pro	Gly	Arg	Ala	Phe	Tyr	Thr	Thr	Gly	Gln	He	116	GIA	ASP	TIE	
	CCA	GGG	AGA	GCA	TTT	TAT	ACA	ACA	GGA	CAA	ATA	ATA	GGA	GAT	AIA	
10																
					35											
	Arg	Gln	Ala	His	Cys											
	AGA	CAA	GCA	CAT	TGT											
15																
	(2)		INFO	RMA'	CION	FOR	SEQ	ID :	NO:	EE62	8-1					
	(-,		(i)		SEQ	UENC	E CH	ARAC	TERI	STIC	s:					
					(A)			GTH:								
					(B)				Nuc1		Acid					
20					(c)		STR	ANDE	DNES	S:	Sing	le				
					(D)				Y:							•
			(ii)	)	KIN	D: c	DNA	to g	enom	ic R	NA					
			(ii		KIN	i) a	f pe	ptid	e or	pro	tein	<b>)</b> :				
			\	•	(A)	-	SEQ	UENC	E AS	SEMB	LY M	<b>ETHO</b>	D:	0ve	lap	
25					(B)				T TY		Int	erna	1 Fr	agme	ent	
					(c)				TICA							
			(ii:	i )	ORI	GINA			: HI							
			(11	-,	(E)		IND	IVI	UAL	ISOL	ATE:					
			(iv	<b>)</b>			TE S									
30			(	,	(C)			NE:		(+)						
			(v)		POS	TTTC			IOME:	Wit	hin	Env	Gene	:		
			(vi		PRO	PERT	TIES	OF S	SEOUE	NCE:	Ė	pres	ses	cons	serve	đ
			(*1	,							ar	tige	mic	det	ermin	ant
			(vi	ii)	SEC	HENC	E DE	SCR	(PTIC	)N:		_				
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	er/	ı ın	NO:	RE6	28-1											
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	Cyt	r ACI	V VCV	CCC	, AA(	· AA'	T AA'	r AC	A AG	A AA	A GG	C AT	A CA	T AT	G GGA	A.
	16.	LAW	1 MGM		, An	, EMI										
45					20	1				2.	5				30	)
	D.	. C1.	, 1	Δ1-	Dh.	o Tu	r A1:	a ፕኮ	r G1			e Il	e Gl	у Ав	n Ile	9
	PT(	A CC	у тур	CU.	7 dada 2 KEI/	- ту Г та	T GC	A AC	A GG	G GA	CAT	A AT	A GG	A AA	T ATA	A
	CC	افاق ۱	אמא ט	. GU	7 11	r ru	_	430								

Arg Gln Ala His Cys AGA CAA GCA CAT TGT INFORMATION FOR SEQ ID NO: EE628-2 (2) SEQUENCE CHARACTERISTICS: (i) LENGTH: 105 (A) TYPE: Nucleic Acid (B) STRANDEDNESS: Single 10 (C) TOPOLOGY: Linear (D) KIND: cDNA to genomic RNA (ii) KIND (if peptide or protein): (ii) SEQUENCE ASSEMBLY METHOD: Overlap (A) FRAGMENT TYPE: Internal Fragment 15 (B) HYPOTHETICAL: (C) ORIGINAL SOURCE: HIV (iii) INDIVIDUAL ISOLATE: IMMEDIATE SOURCE: (iv) CLONE: (C) 20 POSITION IN GENOME: Within Env Gene (v) PROPERTIES OF SEQUENCE: Expresses conserved (vi) antigenic determinant (viii) SEQUENCE DESCRIPTION: SEQ ID NO: EE628-2 15 10 30 1 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His MET Gly TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA GGT ATA CAT ATG GGA 25 20 35 Pro Gly Lys Ala Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asn Ile CCA GGG AAA GCA TIT TAT GCA ACA GGG GAC ATA ATA GGA AAT ATA 40 Arg Gln Ala His Cys AGA CAA GCA CAT TGT INFORMATION FOR SEQ ID NO: EE628-3 (2) 45 SEQUENCE CHARACTERISTICS: (i) LENGTH: 105 (A) TYPE: Nucleic Acid (B) STRANDEDNESS: Single (C)

50

			(D) TOPOLOGY: Linear
		(ii)	KIND: cDNA to genomic RNA
		(ii)	KIND (if peptide or protein):
		<b>\</b> ,	(A) SEQUENCE ASSEMBLY METHOD: Overlap
			(B) FRAGMENT TYPE: Internal Fragment
			(C) HYPOTHETICAL:
. •		(iii)	ORIGINAL SOURCE: HIV
		(111)	(E) INDIVIDUAL ISOLATE:
		(iv)	IMMEDIATE SOURCE:
		(14)	(C) CLONE:
		(v)	POSITION IN GENOME: Within Env Gene
			PROPERTIES OF SEQUENCE: Expresses conserved
		(vi)	
			antigenic determinant
		(viii)	SEQUENCE DESCRIPTION:
	SEQ ID	NO: EE6	i 28–3
	•		
	1		5 10 15
	Cys Thr	Arg Pro	Asn Asn Asn Thr Arg Lys Gly Ile His MET Gly
	TGT ACA	AGA CCC	C AAC AAC AAT ACA AGA AAA GGT ATA CAT ATG GGA
			00 05 70
			20 25 30
			Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asn Ile
	CCA GGG	AAA GCA	TITI TAT GCA ACA GGG GAC ATA ATA GGA AAT ATA
			•
			25
	A 01	A1 - 111 -	35
		Ala His	
	AGA CAA	GCA CAT	. 161
	(2)	TNEODMA	ATION FOR SEQ.ID NO: EE639-1
	(2)	(i)	SEQUENCE CHARACTERISTICS:
		(1)	(A) LENGTH: 105
,			(B) TYPE: Nucleic Acid
			(C) STRANDEDNESS: Single
			(D) TOPOLOGY: Linear
		(44)	·
	1	(ii)	KIND: cDNA to genomic RNA
	,	(ii)	KIND (if peptide or protein):
	*		(A) SEQUENCE ASSEMBLY METHOD: Overlap
			(B) FRACMENT TYPE: Internal Fragment
	•		(C) HYPOTHETICAL:
	· ·	(iii)	ORIGINAL SOURCE: HIV
	:		(E) INDIVIDUAL ISOLATE:
	•	(iv)	IMMEDIATE SOURCE:
	i .		(C) CLONE:

			(v) (vi)						OME : EQUEI		Exp	pres	ses e		erved	
5			(vi	ii)	SEQ	JENCI	E DES	SCRI	PTIOI	٧:	anı	cige	aic (	aetei	rmina	nt
	SEQ	ID I	NO:	EE6	39–1											
10	1				5					10					15	
		Thr	Arg	Pro	_	Asn	His	Thr	G1u		Arg	Ile	Thr	Leu	G1y	
														CTA		
15					20					25					30	
	Pro	Gly	Arg	Val	Leu	Tyr	Thr	Thr	G1y	Arg	Ile	Ile	Gl <b>y</b>	Asp	Ile	
	CCG	GGG	AGA	GTA	CTT	TAT	ACA	ACA	GGA	AGA	ATA	ATA	GGA	GAT	ATA	
20					35											
	Arg	Arg	A1a	His												
	_	_		CAT												
25	(2)		INF	ORMA'	rion	FOR	SEO	ID 1	NO: 1	EE63	9–2					
	(-,		(i)				-		TERI							
,					(A)		LEN	GTH:	10	5						
					(B)		TYP	E: 1	Nucl	eic /	Acid					
30	•				(C)				DNES	_	Sing	le				
					(D)			OLOG		Line						
			(ii	_					enom:			<b>.</b> .				
			(ii	)		D (1:			e or				n	<b>^</b>	1	
					(A) (B)									Over agme		
35					(C)		•		TICA		IHL	er ma	I FL	agme	u c	
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			(	-,	(E)				UAL		ATE:					
			(iv	)	IMM	EDIA'	TE S									
40			•		(C)		CLO	NE:						_		
40			(v)		POS	ITIO	N IN	GEN	OME:	Wit	hin	Env (	Gene			
			(vi	)	PRO	PERT	IES (	OF S	EQUE	NCE:		_			erved rmina	
			iv)	ii)	SEQ	UENC	E DE	SCRI	PTIO	N:						
45																
	SEQ	ID 1	NO:	EE6	39–2											

	(2)	INF	ORMA'	CION	FOR	SEQ	ID I	₩: I	3E639	9–3					
		(i)		SEQU	JENCI	CH/	RAC!	CER IS	STICS	S:					
				(A)		LEN	: HT	105	5						
				<b>(B)</b>		TYPE	: 1	Nucle	eic A	Acid					
20				(C)		STRA	NDE	ONES:	S: 5	Singl	le				
				(D)				<b>?:</b> ]		_					
		(ii	)					enom							
		(ii						or			<b>)</b> :				
		\	•	(A)	-						OHTE	): (	)ver	ар.	
25				(B)		-					rnal				
				(c)				CICA					-6		
		(ii:	i )					HI	_						
		(	-,	(E)				JAL		ATR:					
		(iv	)			CE SO						**			
30		\	,	(C)		CLO									
		(v)			וסנדו			ME:	Witl	nin l	env (	Gene	-		
			)										conse	rved	
			•											mina	at
		(vi	ii)	SEOL	JENCI	Z DES	CRI	PTIO	<b>V</b> :		6				
35		<b>\.</b>	-												
35		(													
35	SEO :			39–3											
35	SEQ :	ID NO:		39–3											
35	SEQ :			39–3											
<b>35</b>	SEQ :			39-3 5					10					15	
	1	ID NO:	EE63	5	Asp	Asn	Thr		10	Ser	Ile	Pro	Ile		
	1 Cys :		EE63	5 Asn				Arg	10 Lys					G1y	
	1 Cys :	ID NO: Thr Arg	EE63	5 Asn				Arg	10 Lys					G1y	
	1 Cys :	ID NO: Thr Arg	EE63	5 Asn				Arg	10 Lys					G1y	
	1 Cys :	ID NO: Thr Arg	EE63	5 Asn				Arg	10 Lys					G1y	
40	1 Cys 1	ID NO: Thr Arg	Pro CCC	5 Asn AAC	AAC	AAT	ACA	Arg AGG	10 <b>Lys</b> AAA 25	AGT	ATA	CCA	ATA	G1y GGA	
40	1 Cys : TGT /	ID NO: Thr Arg ACA AGA	Pro CCC	5 Asn AAC 20 Phe	AAC	AAT Ala	ACA	Arg AGG	10 Lys AAA 25 Asp	AGT Ile	ATA Ile	CCA Gly	ATA Asp	Gly GGA 30 Ile	
40	1 Cys : TGT /	ID NO: Thr Arg ACA AGA	Pro CCC	5 Asn AAC 20 Phe	AAC	AAT Ala	ACA	Arg AGG	10 Lys AAA 25 Asp	AGT Ile	ATA Ile	CCA Gly	ATA Asp	Gly GGA 30 Ile	
40	1 Cys : TGT /	ID NO: Thr Arg ACA AGA	Pro CCC	5 Asn AAC 20 Phe	AAC	AAT Ala	ACA	Arg AGG	10 Lys AAA 25 Asp	AGT Ile	ATA Ile	CCA Gly	ATA Asp	Gly GGA 30 Ile	

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### EP 0 471 407 A2

1 5 10 15

Cys Thr Arg Pro Asn Asn His Thr Glu Lys Arg Ile Thr Leu Gly
TGT ACA AGA CCC AAC AAC CAT ACA GAA AAA CGT ATA ACT CTA GGA

20 25 30

Pro Gly Arg Val Leu Tyr Thr Thr Gly Arg Ile Ile Gly Asp Ile
CCG GGG AGA GTA CTT TAT ACA ACA GGA AGA ATA ATA GGA GAT ATA

35 Arg Arg Ala His Cys AGA CGA GCA CAT TGT

10

5

Arg Gln Ala His Cys

AGA CAA GCA CAT TGT 5 INFORMATION FOR SEQ ID NO: EE660-1 (2) SEQUENCE CHARACTERISTICS: LENGTH: 105 (A) TYPE: Nucleic Acid (B) STRANDEDNESS: Single 10 (C) TOPOLOGY: Linear (D) KIND: cDNA to genomic RNA (ii) KIND (if peptide or protein): (ii) SEQUENCE ASSEMBLY METHOD: Overlap (A) FRAGMENT TYPE: Internal Fragment 15 (B) (C) HYPOTHETICAL: ORIGINAL SOURCE: HIV (iii) INDIVIDUAL ISOLATE: (E) IMMEDIATE SOURCE: (iv) 20 (C) CLONE: POSITION IN GENOME: Within Env Gene (v) PROPERTIES OF SEQUENCE: Expresses conserved (iv) antigenic determinant (viii) SEQUENCE DESCRIPTION: 25 SEQ ID NO: EE660-1 15 30 5 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Pro Ile Gly TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CCT ATA GGA 35 20 Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Val Ile Gly Asp Ile CCA GGA AGA GCA TTT TAT ACA ACA GGA GAT GTA ATA GGA GAT ATA 40 35 Arg Gln Ala Arg Cys AGA CAA GCA CGT TGT (2) INFORMATION FOR SEQ ID NO: EE660-2 (i) SEQUENCE CHARACTERISTICS: LENGTH: 105 (A) TYPE: Nucleic Acid (B) STRANDEDNESS: Single (C)

55

5		(ii) (ii)	(D) TOPOLOGY: Linear KIND: cDNA to genomic RNA KIND (if peptide or protein): (A) SEQUENCE ASSEMBLY METHOD: Overlap (B) FRAGMENT TYPE: Internal Fragment (C) HYPOTHETICAL:
		(iii)	ORIGINAL SOURCE: HIV (E) INDIVIDUAL ISOLATE:
10		(iv)	IMMEDIATE SOURCE: (C) CLONE:
		(v) (vi)	POSITION IN GENOME: Within Env Gene PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
15		(viii)	_
	SEQ ID	NO: EE6	60–2
20	1		5 10 15
	Cys Thr TGT ACA	Arg Pro	Asn Asn Asn Thr Arg Arg Ser Ile Asn Ile Gly AAC AAC AAT ACA AGA AGA AGT ATA AAT ATA GGA
25			20 25 30
	Pro Gly CCA GGG	Arg Ala AGA GCA	Phe Tyr Ala Thr Gly Ala Ile Ile Gly Asp Ile TTC TAT GCA ACA GGA GCC ATA ATA GGA GAT ATA
30			<b>35</b>
	-	Ala His GCA CAT	- ·
35	(2)		TION FOR SEQ ID NO: EE661-1
		(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 105  (B) TYPE: Nucleic Acid  (C) CTRANDEDNESS: Size10
40		(ii)	(C) STRANDEDNESS: Single (D) TOPOLOGY: Linear KIND: cDNA to genomic RNA
		(ii)	KIND (if peptide or protein): (A) SEQUENCE ASSEMBLY METHOD: Overlap (B) FRAGMENT TYPE: Internal Fragment
45		(iii)	(C) HYPOTHETICAL: ORIGINAL SOURCE: HIV (E) INDIVIDUAL ISOLATE:
		(iv)	IMMEDIATE SOURCE: (C) CLONE:

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Cys	Thr	Arg	Pro	ASI	ASD	ASI	THE	Arg AGA	TAR	VC1.	ATA	CAT	ATA	GGA
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Pro	G1 v	Arg	Ala		Tvr	Ala	Thr	Gly	Glu	Ile	Ile	G1y	Авр	Ile
CCA	GGG	AGA	GCA	TTT	TAT	GCA	ACA	GGA	GAA	ATA	ATA	GGA	GAT	ATA
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				(B)		TYP		Nucl	_	Acid				
				(c)				DNES						
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		(vi	ii)	SEQ	UENC	E DE	SCRI	PTIO	N:		<b>5</b> -			

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		Thr	Arg	Pro		Asn	Asn	Thr	Arg	Lys	Ser	Ile	His	I1e	G1y	
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	Pro	G1y	Arg	Ala	Phe	Tyr	Ala	Thr	G1y	G1u	Ile	Ile	Gly	Asp	Ile	
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	Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile	Ser	Ile	Gly	
	TGT	ACA	AGA	CCC	AAC	AAC	AAT	ACA	AGA	AAA	AGT	ATA	TCT	ATA	GGA	
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	CCA	GGG	AGA	GCA	TTT	TTT	ACA	AUA	GGA	UAA	ATA	ATA	GGA	GAI	ATA	

	Arg Gln A AGA CAA G	la His Cys CA CAT TGT	
5			
		i) SEQUENCE (A) (B)	SEQ ID NO: EE663-1 CHARACTERISTICS: LENGTH: 105 TYPE: Nucleic Acid
10		(C)	STRANDEDNESS: Single TOPOLOGY: Linear
15		(ii) KIND: cD (ii) KIND (if (A)	NA to genomic RNA  peptide or protein): SEQUENCE ASSEMBLY METHOD: Overlap FRAGMENT TYPE: Internal Fragment
		(c)	HYPOTHETICAL:
	(	(iii) ORIGINAL	SOURCE: HIV INDIVIDUAL ISOLATE:
	(	(iv) IMMEDIAT	E SOURCE:
20			CLONE: IN GENOME: Within Env Gene
		(v) POSITION (vi) PROPERTI	ES OF SEQUENCE: Expresses conserved antigenic determinant
25	•	(viii) SEQUENCE	DESCRIPTION:
	SEQ ID NO	O: EE663-1	
30	`1	5	10 15
	Over The	Arg Pro Asn Asn	Asn Thr Arg Lys Ser Ile Thr Ile Gly AAT ACA AGA AAA AGT ATA ACT ATA GGA
35		20	. 25 30
	Pro Gly (	Are Ala Phe Tvr	Ala Thr Gly Glu Ile Ile Gly Asp Ile GCA ACA GGA GAA ATA ATA GGA GAT ATA
40		35	
	Arg Gln	Ala His Cys	·
		GCA CAT TGT	·
45	(2)	INFORMATION FOR (i) SEQUENC (A) (B) (C)	SEQ ID NO: EE663-2 E CHARACTERISTICS: LENGTH: 105 TYPE: Nucleic Acid STRANDEDNESS: Single

			(D) TOPOLOGY: Linear
		(ii)	KIND: cDNA to genomic RNA
		(ii)	KIND (if peptide or protein):
5		(11)	(A) SEQUENCE ASSEMBLY METHOD: Overlap
•			(B) FRAGMENT TYPE: Internal Fragment
			(C) HYPOTHETICAL:
		(iii)	ORIGINAL SOURCE: HIV
		(111)	(E) INDIVIDUAL ISOLATE:
10		(:)	IMMEDIATE SOURCE:
10		(iv)	
		()	(C) CLONE: POSITION IN GENOME: Within Env Gene
		(v)	PROPERTIES OF SEQUENCE: Expresses conserved
		(vi)	antigenic determinant
		(!!!)	_
15		(V111)	SEQUENCE DESCRIPTION:
	CEO ID	NO. PEG	42 2
	SEQ ID	NO: EE6	03-2
20			
20	1		5 10 15
		Ara Dra	Asn Asn Asn Thr Arg Lys Gly Ile His Ile Gly
	TOT ACA	ACA CCC	AAC AAC AAT ACA AGA AAA GGT ATA CAT ATA GGA
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25			
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	D=0 C1=	. 450 410	Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asn Ile
	COA CCC	YCY CCY	TIT TAT ACA ACA GGA GAA ATA ATA GGA AAT ATA
	COA GGG	AGA GCA	III IAI AOA AOA GGA GAN AIN AIN AOA IMI
50	•		
50			35
	Ara Gla	Ala His	
	-	GCA CAT	
	AGA CAR	GON ONL	101
35			
30	(2)	TNFORMA	TION FOR SEQ ID NO: EE663-3
	(2)	(i)	SEQUENCE CHARACTERISTICS:
		(1)	(A) LENGTH: 105
			(B) TYPE: Nucleic Acid
40			(C) STRANDEDNESS: Single
70			(D) TOPOLOGY: Linear
		(ii)	KIND: cDNA to genomic RNA
		(ii)	KIND (if peptide or protein):
		(11)	(A) SEQUENCE ASSEMBLY METHOD: Overlap
15			(B) FRACMENT TYPE: Internal Fragment
45			(C) HYPOTHETICAL:
		(iii)	ORIGINAL SOURCE: HIV
		(111)	(E) INDIVIDUAL ISOLATE:
		(4)	IMMEDIATE SOURCE:
		(iv)	
50			(C) CLONE:

		(v) (vi)		POSITION IN GENOME: Within Env Gene PROPERTIES OF SEQUENCE: Expresses conserved antigenic determins
		(vi	ii)	
SEQ	ID I	10:	EE6	53–3
1				5 10 15
Cys	Thr	Arg	Pro	Asn Asn Asn Thr Ile Lys Ser Ile Thr Ile Gly
TGT	ACA	AGA	CCC	AAC AAC AAT ACA ATA AAA AGT ATA ACT ATA GGA
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	_			20 25 30
Pro	Gly	Arg	Ala	Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile
CCA	GGG	AGA	GCA	TIT TAT GCA ACA GGA GAA ATA ATA GGA GAT ATA
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	<b>01</b>	41-	TT 4 -	35
_	Gln CAA			
AGA	UAA	GUA	CAI	161
(2)		TNE	ODMA'	TION FOR SEQ ID NO: EE665-1
(2)		(i)	JIG IA	SEQUENCE CHARACTERISTICS:
		(1)		(A) LENGTH: 105
				(B) TYPE: Nucleic Acid
				(C) STRANDEDNESS: Single
				(D) TOPOLOGY: Linear
		(ii	)	KIND: cDNA to genomic RNA
		(ii	)	KIND (if peptide or protein):
				(A) SEQUENCE ASSEMBLY METHOD: Overlap
				(B) FRACMENT TYPE: Internal Fragment
				(C) HYPOTHETICAL:
		(ii	i)	ORIGINAL SOURCE: HIV
		,.		(E) INDIVIDUAL ISOLATE:
		(iv	)	IMMEDIATE SOURCE:
		( <b>x</b>		(C) CLONE:
		(v)		POSITION IN GENOME: Within Env Gene PROPERTIES OF SEQUENCE: Expresses conserve
		(vi	,	PROPERTIES OF SEQUENCE: Expresses conserved antigenic determination
		(vi	ii)	SEQUENCE DESCRIPTION:
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	1				5					10					15	
	Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Arg	Ser	Ile	Pro	Ile	Gly	
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	Pro	GLY	Arg	Ala GCA	PDE	TAT	ATS	TUL	CCA	GID	TIE	TIG	CCA	CAT	ATA	
	CCA	666	AGA	GUA	111	TWI	GUA	MUM	GGA	UAA	um	VIV	GGEA	GIN	um	
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40		ID I	10:	EE6						10					15	
40	1				5	Acn	Acn	The	Ara	10 Ara	Sor	Tle	Pro	T1e	15	
40	1 Cys	Thr	Arg	Pro	5 Asn					Arg					G1y	
40	1 Cys	Thr	Arg		5 Asn					Arg					G1y	
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<b>4</b> 0 <b>4</b> 5	1 Cys	Thr	Arg	Pro	5 Asn					Arg					G1y	
	1 Cys TGT	Thr ACA	Arg AGA	Pro CCC	5 Asn AAC 20 Phe	AAC	AAT	ACA	AGA Gly	Arg AGA 25 Gln	AGT Ile	ATA Ile	CCT	ATA	Gly GGA 30 Ile	
	1 Cys TGT	Thr ACA	Arg AGA	Pro CCC	5 Asn AAC 20 Phe	AAC	AAT	ACA	AGA Gly	Arg AGA 25 Gln	AGT Ile	ATA Ile	CCT	ATA	Gly GGA 30 Ile	
	1 Cys TGT	Thr ACA	Arg AGA	Pro CCC	5 Asn AAC 20 Phe	AAC	AAT	ACA	AGA Gly	Arg AGA 25 Gln	AGT Ile	ATA Ile	CCT	ATA	Gly GGA 30 Ile	

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30	1				5					10					15	
30	1 Cys	Thr	Arg	Pro	5 Asn	Asn	Asn	Thr	Arg	Arg	Ser	Ile	Pro	Ile	Gly	
<b>30</b>	1 Cys	Thr	Arg	Pro	5 Asn	Asn AAC	Asn AAT	Thr ACA	Arg AGA	Arg	Ser AGT	Ile ATA	Pro CCT	Ile ATA	Gly	
30	1 Cys	Thr	Arg	Pro	5 Asn	Asn AAC	Asn AAT	Thr ACA	Arg AGA	Arg	Ser AGT	Ile ATA	Pro CCT	Ile ATA	Gly	
30	1 Cys	Thr	Arg	Pro	5 Asn	Asn AAC	Asn AAT	Thr ACA	Arg AGA	Arg AGA	Ser AGT	Ile ATA	Pro CCT	Ile ATA	G1y GGA	
	1 Cys TGT	Thr ACA	Arg AGA	Pro CCC	5 Asn AAC	AAC	AAT	ACA	AGA	Arg AGA	AGT	ATA	CCT	ATA	G1y GGA	
	1 Cys TGT	Thr ACA	Arg AGA	Pro CCC	5 Asn AAC 20 Phe	AAC	AAT	ACA	AGA G1y	Arg AGA 25 Gln	AGT Ile	ATA Ile	CCT Gly	ATA Asp	Gly GGA 30 Ile	
	1 Cys TGT	Thr ACA	Arg AGA	Pro CCC	5 Asn AAC 20 Phe	AAC	AAT	ACA	AGA G1y	Arg AGA 25 Gln	AGT	ATA Ile	CCT Gly	ATA Asp	Gly GGA 30 Ile	
	1 Cys TGT	Thr ACA	Arg AGA	Pro CCC	5 Asn AAC 20 Phe	AAC	AAT	ACA	AGA G1y	Arg AGA 25 Gln	AGT Ile	ATA Ile	CCT Gly	ATA Asp	Gly GGA 30 Ile	
	1 Cys TGT	Thr ACA	Arg AGA	Pro CCC	5 Asn AAC 20 Phe	AAC	AAT	ACA	AGA G1y	Arg AGA 25 Gln	AGT Ile	ATA Ile	CCT Gly	ATA Asp	Gly GGA 30 Ile	
35	1 Cys TGT	Thr ACA	Arg AGA	Pro CCC	5 Asn AAC 20 Phe	AAC	AAT	ACA	AGA G1y	Arg AGA 25 Gln	AGT Ile	ATA Ile	CCT Gly	ATA Asp	Gly GGA 30 Ile	
35	1 Cys TGT Pro CCA	Thr ACA Gly GGG	Arg AGA Arg AGA	Pro CCC	5 Asn AAC 20 Phe TTT	AAC	AAT	ACA	AGA G1y	Arg AGA 25 Gln	AGT Ile	ATA Ile	CCT Gly	ATA Asp	Gly GGA 30 Ile	
35	1 Cys TGT Pro CCA	Thr ACA Gly GGG	Arg AGA Arg AGA	Pro CCC Ala GCA	5 Asn AAC 20 Phe TTT 35 Cys	AAC	AAT	ACA	AGA G1y	Arg AGA 25 Gln	AGT Ile	ATA Ile	CCT Gly	ATA Asp	Gly GGA 30 Ile	
35	1 Cys TGT Pro CCA	Thr ACA Gly GGG	Arg AGA Arg AGA	Pro CCC Ala GCA	5 Asn AAC 20 Phe TTT 35 Cys	AAC	AAT	ACA	AGA G1y	Arg AGA 25 Gln	AGT Ile	ATA Ile	CCT Gly	ATA Asp	Gly GGA 30 Ile	
35	1 Cys TGT Pro CCA	Thr ACA Gly GGG	Arg AGA Arg AGA	Pro CCC Ala GCA	5 Asn AAC 20 Phe TTT 35 Cys	AAC	AAT	ACA	AGA G1y	Arg AGA 25 Gln	AGT Ile	ATA Ile	CCT Gly	ATA Asp	Gly GGA 30 Ile	
35 40	1 Cys TGT Pro CCA	Thr ACA Gly GGG	Arg AGA Arg AGA	Pro CCC Ala GCA His CAT	5 Asn AAC 20 Phe TTT 35 Cys	Tyr TAT	Ala GCA	Thr ACA	G1y GGA	Arg AGA 25 Gln CAA	Ile ATA	ATA Ile	CCT Gly	ATA Asp	Gly GGA 30 Ile	
35 40	1 Cys TGT Pro CCA	Thr ACA Gly GGG	Arg AGA Arg AGA	Pro CCC Ala GCA His CAT	5 Asn AAC 20 Phe TTT 35 Cys TGT	Tyr TAT	Ala GCA	Thr ACA	G1y GGA	Arg AGA 25 Gln CAA	Ile ATA	ATA Ile	CCT Gly	ATA Asp	Gly GGA 30 Ile	
35 40	1 Cys TGT Pro CCA	Thr ACA Gly GGG	Arg AGA Arg AGA Ala GCA	Pro CCC Ala GCA His CAT	5 Asn AAC 20 Phe TTT 35 Cys TGT	Tyr TAT	Ala GCA SEQ E CH	Thr ACA	G1y GGA	Arg AGA 25 Gln CAA	Ile ATA	ATA Ile	CCT Gly	ATA Asp	Gly GGA 30 Ile	
35 40	1 Cys TGT Pro CCA	Thr ACA Gly GGG	Arg AGA Arg AGA Ala GCA	Pro CCC Ala GCA His CAT	5 Asn AAC 20 Phe TTT 35 Cys TGT	Tyr TAT	AAT Ala GCA SEQ E CH	Thr ACA  ID I	Gly GGA NO: 1 TERIS	Arg AGA 25 Gln CAA EE66 STIC	Ile ATA	ATA Ile	CCT Gly	ATA Asp	Gly GGA 30 Ile	
35	1 Cys TGT Pro CCA	Thr ACA Gly GGG	Arg AGA Arg AGA Ala GCA	Pro CCC Ala GCA His CAT	5 Asn AAC 20 Phe TTT 35 Cys TGT	Tyr TAT	AAT Ala GCA SEQ E CHA LENG TYP	Thr ACA  ID I	G1y GGA	Arg AGA 25 Gln CAA EE66 STIC	Ile ATA	Ile ATA	CCT Gly	ATA Asp	Gly GGA 30 Ile	

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1				5					10					15
	The	Ara	Pro		Aen	Aen	Thr	Aro		Aro	T1e	Thr	Thr	
TGT	ACA	AGA	CCC	AAC	AAC	AAT	ACA	AGA	AAA	AGA	ATA	ACT	ACG	GGA
				20					25					30
Pro	G1y	Arg	Va1	Tyr	Tyr	Thr	Thr	G1y	Asp	Ile	I1e	Gly	Asp	I1e
CCG	GGG	AGĀ	GTA	TAT	TAT	ACA	ACA	GGA	GAT	ATA	ATA	GGA	GAT	ATA
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	(v) (vi)	POSITION IN GENOME: Within Env Gene PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
5	(viii)	
	SEQ ID NO: EE6	67–2
10	1 Cys Thr Arg Pro TGT ACA AGA CCC	5 10 15 Ser Asn Asn Thr Arg Lys Ser Ile His Ile Gly AGC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA
15	Pro Gly Arg Ala CCA GGG AGA GCA	20 25 30 Phe Tyr Thr Thr Gly Glu Ile Ile Glu Asn Ile TTT TAT ACA ACA GGA GAA ATA ATA GAA AAT ATA
20	Arg Gln Ala His AGA CAA GCA CAC	
25	(2) INFORMA	TION FOR SEQ ID NO: EE667-3 SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 (B) TYPE: Nucleic Acid
30	(ii) (ii)	(C) STRANDEDNESS: Single (D) TOPOLOGY: Linear KIND: cDNA to genomic RNA KIND (if peptide or protein): (A) SEQUENCE ASSEMBLY METHOD: Overlap (B) FRACMENT TYPE: Internal Fragment
35	(iii)	(C) HYPOTHETICAL: ORIGINAL SOURCE: HIV (E) INDIVIDUAL ISOLATE:
40	(iv) (v) (vi)	IMMEDIATE SOURCE:  (C) CLONE:  POSITION IN GENOME: Within Env Gene PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
45		SEQUENCE DESCRIPTION:
50		5 10 15 Ser Asn Asn Thr Arg Lys Ser Ile His Ile Ala C AGC AAC AAT ACA AGA AAA AGT ATA CAT ATA GCA

					20					25					30	
	Pro	G1y	Arg	A1a	Phe	Tyr	Thr	Thr	G1y	Glu	Ile	I1e	G1u	Asn	I1e	
	CCA	GGG	AGA	<b>GCA</b>	TTT	TAT	ACA	ACA	GGA	GAA	ATA	ATA	GAA	AAT	ATA	
5																
					35											
	Arg	G1n	Ala	His	Cys											
	_			CAC												
10																
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	(2)		INF	ORMA!	CION	FOR	SEQ	ID I	NO: 1	EE669	<del>-</del> 1					
			(i)		SEQ	JENC	E CHA	ARAC:	TER IS	STICS	3:					
					(A)		LEN(	STH:	10	5						
15					(B)		TYPI	Z: 1	Nucle	eic A	cid					
					(C)		STRA	ANDE	DNES:	s: s	Sing	le				
					(D)		TOP	LOG	Y: 1	Linea	ar					
			(ii)	)			DNA 1	to g	enom	ic Ri	NA.					
			(ii							prot		):				
20			•	-	(A)	•				SEMBI			): (	)ver]	lap	
					(B)				r TY				l Fra			
					(c)		HYPO	THE:	rica:	ւ։ _						
			(ii:	i)		GINA:	L SOI	JRCE	: HIV	7						
				•	(E)					ISOL	ATE:					
25			(iv	)	IMM	EDIA'	TE S									
			•	•	(C)		CLO	VE:						_		
			(v)		POS	ITIO	N IN	GEN	OME:	With	nin 1	Inv (	Gene			
			(vi											conse	erved	
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30	,		(vi:	ii)	SEQ	UENC	E DES	SCRI	PTIO	<b>V</b> :		_				
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	SEQ	ID I	:00	EE6	69-1											
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35																
	1				5					10					15	
										Lys						
	TGT	ACA	AGA	CCT	AAC	AAC	AAT	ACA	AGA	AAA	AGT	ATA	CCT	ATA	GGA	
40																
					20					25					30	
										G1u						
	CCA	GGG	AGA	GCA	ATT	TAT	GCA	ACA	GGA	GAA	ATA	ATA	GGA	GAT	ATA	
45																
					35											
	Arg	G1n	Ala	His	Cys											
	AGA	CAA	GCA	CAT	TGT											
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	(2)		INF(	ORMA'	CION	FOR	SEQ	ID P	NO: 1	EE66	9-2		•			
			(i)		SEO	UENC	E CH	ARAC?	CER IS	STIC	S:					
			<b>\</b> -,		(A)		LEN		10							
5					(B)		TYPI		luc1e	eic A	Acid					
					(c)			NDEI			Singl	le				
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15			(iv)	,		EDIA:		OURCE	<b>5</b>							
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			(v)					GENC								
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20			(vii	li)	SEQ	UENCI	C DES	SCRIF	TIOI	<b>v:</b>						
	SEQ :	ID N	10:	EE66	9-2											
25	_				_										16	
	1			_	. 5		_			_10	_		_		15	
	Cys :															
	TGT A	ACA	AGA	CCT	AAC	AAC	AAT	ACA	AGA	AAA	AGT	ATA	CCT	ATA	GGA	
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	Pro															
	CCA	GGG	AGA	GCA	ATT	TAT	GCA	ACA	GGA	GAA	ATA	ATA	GGA	GAT	ATA	
35																
					35											
	Arg															
	AGA (	CAA	GCA	CAT	TGT											
40	4-5															
	(2)			)RMA				ID N								
			(i)			UENCI		ARAC'		_	3:					
					(A)			STH:	10:							
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45					(c)			ANDEI			Singl	le				
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			(ii)					to ge								
			(ii)	)		D (i		ptide						_		
					(A)		-	JENCI						Over1	-	
50					(B)		FRA	MEN.	TYI	PE:	Inte	erna	l Fr	agmen	ıt	

		(C) HYPOTHETICAL:
	(iii)	ORIGINAL SOURCE: HIV
	(222)	(E) INDIVIDUAL ISOLATE:
5	(iv)	IMMEDIATE SOURCE:
	(20)	(C) CLONE:
	(v)	POSITION IN GENOME: Within Env Gene
		PROPERTIES OF SEQUENCE: Expresses conserved
	(vi)	antigenic determinant
10	(:::1)	
	(viii)	SEQUENCE DESCRIPTION:
	OPO TO NO. PPA	cco 2
	SEQ ID NO: EE6	669–3
15		
13		- 10
	1	5 10 15
	Cys Thr Arg Pro	o Asn Asn Asn Thr Arg Lys Ser Ile Pro Ile Gly
	TGT ACA AGA CC	T AAC AAC AAT ACA AGA AAA AGT ATA CCT ATA GGA
20	•	
		20 25 30
	Pro Gly Arg Ala	a Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asp Ile
	CCA GGG AGA GCA	A TTT TAT ACA ACA GGA GAA ATA ATA GGA GAT ATA
25		•
		35
	Arg Gln Ala His	s Cys
	AGA CAA GCA CAT	T TGT
30		•
	(2) INFORMA	ATION FOR SEQ ID NO: EE1476-1
	(i)	SEQUENCE CHARACTERISTICS:
	ν-/	(A) LENGTH: 102
		(B) TYPE: Nucleic Acid
35	•	(C) STRANDEDNESS: Single
		(D) TOPOLOGY: Linear
	(ii)	KIND: cDNA to genomic RNA
	(ii)	KIND (if peptide or protein):
	\/	(A) SEQUENCE ASSEMBLY METHOD: Overlap
40		(B) FRACMENT TYPE: Internal Fragment
		(C) HYPOTHETICAL:
	(iii)	ORIGINAL SOURCE: HIV
	(111)	(E) INDIVIDUAL ISOLATE:
	(4)	IMMEDIATE SOURCE:
45	(iv)	
<b>~~</b>		(C) CLONE:
	(v)	POSITION IN GENOME: Within Env Gene
	(vi)	PROPERTIES OF SEQUENCE: Expresses conserved
:	,	antigenic determinant
:	(viii)	SEQUENCE DESCRIPTION:

SEQ ID NO: EE1476-1 5 5 10 1 Cys Thr Arg Pro Tyr Asn Asn Ile Lys Ile Arg Ser Ile His Ile TGT ACA AGG CCC TAC AAC AAT ATA AAA ATA AGA AGT ATA CAT ATA 30 10 20 Gly Pro Gly Arg Pro Phe Tyr Thr Thr Lys Ile Gly Asp Ile Arg GGA CCA GGG AGA CCA TTT TAT ACA ACA AAA ATA GGA GAT ATA AGA 15 35 Gln Ala Tyr Cys CAA GCA TAT TGT 20 INFORMATION FOR SEQ ID NO: EE3032-1 (2) SEQUENCE CHARACTERISTICS: LENGTH: 105 (A) TYPE: Nucleic Acid (B) STRANDEDNESS: Single (C) 25 TOPOLOGY: Linear (D) KIND: cDNA to genomic RNA (ii) (ii) KIND (if peptide or protein): (A) SEQUENCE ASSEMBLY METHOD: Overlap FRACMENT TYPE: Internal Fragment (B) 30 HYPOTHETICAL: (C) (iii) ORIGINAL SOURCE: HIV (E) INDIVIDUAL ISOLATE: (iv) IMMEDIATE SOURCE: CLONE: (C) POSITION IN GENOME: Within Env Gene 35 (v) PROPERTIES OF SEQUENCE: Expresses conserved (vi) antigenic determinant (viii) SEQUENCE DESCRIPTION: 40 SEQ ID NO: EE3032-1 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly 45 TGT ACA AGG CCC AAT AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

55

Pro Gly Arg Ala Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile CCA GGG AGG GCA TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA

					35										
	Arg	Gln	Ala	His	Cys										
			GCA												
5															
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			(1)		(A)	, mior	LENG		105	_	•				
10					(B)		TYPE		lucle		hio				
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15					(A)		-							ver1	
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					(C)				CICAL						
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20			(iv)	)		CAID	CE SC		ß:						
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			(v)								nin F				_
			(vi)	)	PRO	ERT!	CES C	F SE	EQUEN	ICE:					rved
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25			(vii	ii)	SEQU	JENCI	Z DES	CRI	(OIT	<b>1</b> :					
	SEQ	ID I	: 07	EE30	)32–2	2									
30															
	1				5					10					15
	Cvs	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Gly	Ile	His	MET	G1y
	TGT	ACA	AGG	CCC	AAT	AAC	AAT	ACA	AGA	AAA	GGT	ATA	CAT	ATG	GGA
35															
					20					25					30
	Pro	G1v	Arg	Ala	Phe	T√t	Thr	Thr	G1y	Asp	Ile	Ile	G1y	Asp	Ile
	CCA	GGG	AGG	GCA	TTT	TAT	ACA	ACA	GGA	GAC	ATA	ATA	GGA	GAT	ATA
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			GCA												
	NGA	UAA	GCA	ONI	101										
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	(2)			ORMA'											
			(i)			UENC.			TERI		o :				
					(A)			GTH:							
					(B)		TYP		Nuc1			1 _			
50					(C)		STR	ande:	DNES	s: :	Sing	те			

5		(ii) (ii)	(D) TOPOLOGY: Linear KIND: cDNA to genomic RNA KIND (if peptide or protein): (A) SEQUENCE ASSEMBLY METHOD: Overlap (B) FRACMENT TYPE: Internal Fragment (C) HYPOTHETICAL:
		(iii)	ORIGINAL SOURCE: HIV (E) INDIVIDUAL ISOLATE:
10		(iv)	IMMEDIATE SOURCE: (C) CLONE:
		(v) (vi)	POSITION IN GENOME: Within Env Gene PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant
15		(viii)	SEQUENCE DESCRIPTION:
	SEQ ID	NO: EE3	032–3
20	1		5 10 15
	Cys Th	r Arg Pro	Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly
	TGT AC	A AGG CCC	AAT AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA
25			20 25 30
			Phe Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile
	CCA GG	G AGG GCA	TTT TAT ACA ACA GGA GAC ATA ATA GGA GAT ATA
30			35
	Arg Gl	n Ala His	
	AGA CA	A GCA CAT	TGT
35	(2)	INFORMA	TION FOR SEQ ID NO: EEE6405-1
	<b>,</b> -,	(i)	SEQUENCE CHARACTERISTICS:
			(A) LENGTH: 105
			(B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single
40			(D) TOPOLOGY: Linear
-		(ii)	KIND: cDNA to genomic RNA
		(ii)	KIND (if peptide or protein):
			(A) SEQUENCE ASSEMBLY METHOD: Overlap (B) FRACMENT TYPE: Internal Fragment
45			(C) HYPOTHETICAL:
		(iii)	ORIGINAL SOURCE: HIV
		(iv)	(E) INDIVIDUAL ISOLATE:
		(2.7)	(C) CLONE:
50		(w)	POSITION IN GENOME: Within Env Gene

					20					25					30	
	Pro	G1v	Arg	Ala		Tyr	Ala	Thr	Gly	G1u	Ile	MET	Gly	Asp	Ile	
	CCA	GGG	AGA	GCA	TTT	TAT	GCA	ACA	GGA	GAA	ATA	ATG	GGA	GAT	ATA	
5																
					35											
				His												
	AGA	CAA	GCA	CAT	TGT											
10																
-	(2)		INF	ORMA:	rton	FOR	SEO	TD B	io: F	EE640	)5–3					
	(2)		(i)	J.W.Z.			E CHA									
			(-)		(A)		LEN		105							
					(B)				Nucle	ic A	Acid					
15					(c)		STR	NDE	)NES	s: S	Sing	le				
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			(v)		POS	TTO	N TN		ME:	Witl	nin l	Env (	Gene	-	-	
			(v) (vi				N IN	GEN							erved	
· .			(v) (vi					GEN			Exp	pres	ses (	cons	erved minan	t
			iv)		PRO	PERT	IES (	GENO OF SI	SQUEI	VCE:	Exp	pres	ses (	cons		t
30			iv)	)	PRO	PERT	IES (	GENO OF SI	SQUEI	VCE:	Exp	pres	ses (	cons		t
30			(vi (vi	) ii)	PRO	PERT	IES (	GENO OF SI	SQUEI	VCE:	Exp	pres	ses (	cons		t
30	SEQ	ID 1	(vi (vi	)	PRO	PERT	IES (	GENO OF SI	SQUEI	VCE:	Exp	pres	ses (	cons		ţ
30	SEQ	ID 1	(vi (vi	) ii)	PRO	PERT	IES (	GENO OF SI	SQUEI	VCE:	Exp	pres	ses (	cons		ţ.
		ÎD 1	(vi (vi	) ii)	PROD SEQ!	PERT	IES (	GENO OF SI	SQUEI	VCE:	Exp	pres	ses (	cons	rminan	t
30	1		(vi (vi:	) ii) EE6	PRO1 SEQ1 405-	PERT JENC	ies (	GEN( OF SI	SQUE	VCE: V:	Exp	press tige	ses (	conse deter	rminan 15	t
	1 Сув	Thr	(vi (vi: NO:	) ii) EE6	PROD SEQUATION SEQUENTS 405-2 Asn	PERT JENC 3	IES ( E DE: Asn	GEN( OF SI SCRII	PTIOI Arg	NCE: N: 10 Lys	Expan	press tiges	ses o	conse deter	minan 15 Gly	ţ <b>t</b>
	1 Сув	Thr	(vi (vi: NO:	) ii) EE6	PROD SEQUATION SEQUENTS 405-2 Asn	PERT JENC 3	IES ( E DE: Asn	GEN( OF SI SCRII	PTION Arg	NCE: N: 10 Lys	Expan	press tiges	ses (	conse deter	minan 15 Gly	t
	1 Сув	Thr	(vi (vi: NO:	) ii) EE6	PROD SEQUATION SEQUENTS 405-2 Asn	PERT JENC 3	IES ( E DE: Asn	GEN( OF SI SCRII	PTION Arg	NCE: N: 10 Lys	Expan	press tiges	ses (	conse deter	minan 15 Gly	t
	1 Cys TGT	Thr ACA	(vi (vi: NO: Arg AGA	) ii) EE6 Pro	PROD SEQUATION SEQUATION SEQUENTIAL SEQUENTI	PERT JENC 3 Asn AAC	Asn AAT	GENG OF SI SCRII	PTION PTION Arg AGG	IO Lys AAA	Exp and Ser AGT	press tiges Ile ATA	Pro CCT	Ile ATA	15 G1y GGA	t
35	1 Cys TGT	Thr ACA Arg	(vi (vi NO: Arg AGA	) ii) EE6 Pro CCC	PROD SEQUATION SEQUENTS AS	PERT UENC	Asn AAT	GENGOF SI SCRII	Arg AGG	IO Lys AAA 25 Asp	Expanded Ser AGT	Ile ATA	Pro CCT	Ile ATA	15 Gly GGA 30 Ile	t
35	1 Cys TGT	Thr ACA Arg	(vi (vi NO: Arg AGA	) ii) EE6 Pro	PROD SEQUATION SEQUENTS AS	PERT  JENC  Asn AAC	Asn AAT	GENGOF SI SCRII	Arg AGG	IO Lys AAA 25 Asp	Expanded Ser AGT	Ile ATA	Pro CCT	Ile ATA	15 Gly GGA 30 Ile	t
35	1 Cys TGT	Thr ACA Arg	(vi (vi NO: Arg AGA	) ii) EE6 Pro CCC	PROD SEQUATION SEQUENTS AS	PERT  JENC  Asn AAC	Asn AAT	GENGOF SI SCRII	Arg AGG	IO Lys AAA 25 Asp	Expanded Ser AGT	Ile ATA	Pro CCT	Ile ATA	15 Gly GGA 30 Ile	t
35 40	1 Cys TGT	Thr ACA Arg	(vi (vi NO: Arg AGA	) ii) EE6 Pro CCC	PROF SEQUATE SEQUENT S	PERT  JENC  Asn AAC	Asn AAT	GENGOF SI SCRII	Arg AGG	IO Lys AAA 25 Asp	Expanded Ser AGT	Ile ATA	Pro CCT	Ile ATA	15 Gly GGA 30 Ile	t
35	1 Cys TGT Pro	Thr ACA Arg AGG	(vi (vi NO: Arg AGA	) ii) EE6 Pro CCC	PROP SEQUATE SEQUENTS AS AS A AAC 20 Phe TTT 35	PERT  JENC  Asn AAC	Asn AAT	GENGOF SI SCRII	Arg AGG	IO Lys AAA 25 Asp	Expanded Ser AGT	Ile ATA	Pro CCT	Ile ATA	15 Gly GGA 30 Ile	t
35 40	1 Cys TGT Pro CCA	Thr ACA Arg AGG	(vi (vi (vi NO: Arg AGA	) ii) EE66 Pro CCC Ala GCA	PROD SEQUADO - S 405 - S Asn AAC 20 Phe TTT 35 Cys	PERT  JENC  Asn AAC	Asn AAT	GENGOF SI SCRII	Arg AGG	IO Lys AAA 25 Asp	Expanded Ser AGT	Ile ATA	Pro CCT	Ile ATA	15 Gly GGA 30 Ile	t
35 40	1 Cys TGT Pro CCA	Thr ACA Arg AGG	(vi (vi (vi NO: Arg AGA	) ii) EE6 Pro CCC	PROD SEQUADO - S 405 - S Asn AAC 20 Phe TTT 35 Cys	PERT  JENC  Asn AAC	Asn AAT	GENGOF SI SCRII	Arg AGG	IO Lys AAA 25 Asp	Expanded Ser AGT	Ile ATA	Pro CCT	Ile ATA	15 Gly GGA 30 Ile	t

5	(2)	(ii) (iii) (iii)	TION FOR SEQ ID NO: EE6636-1  SEQUENCE CHARACTERISTICS:  (A) LENGTH: 105  (B) TYPE: Nucleic Acid  (C) STRANDEDNESS: Single  (D) TOPOLOGY: Linear  KIND: cDNA to genomic RNA  KIND (if peptide or protein):  (A) SEQUENCE ASSEMBLY METHOD: Overlap  (B) FRAGMENT TYPE: Internal Fragment  (C) HYPOTHETICAL:  ORIGINAL SOURCE: HIV  (E) INDIVIDUAL ISOLATE:								
15		(iv) (v) (vi)	IMMEDIATE SOURCE:  (C) CLONE:  POSITION IN GENOME: Within Env Gene PROPERTIES OF SEQUENCE: Expresses conserved antigenic determinant								
20		(viii)	SEQUENCE DESCRIPTION:								
	SEQ ID	NO: EE6	636–1								
25	1 Cys Th TGT AC	r Arg Pro A AGA CCC	5 10 15 Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA								
30	Pro Gl	y Arg Ala C AGA GCA	20 25 30 Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asn Ile TTT TAT ACA ACA GGA GAA ATA ATA GGA AAT ATA								
<b>35</b>	Arg Gl	n Ala His	35 Cys								
40	AGA CA	A GCA CAT INFORMA (i)	TION FOR SEQ ID NO: EE6636-2 SEQUENCE CHARACTERISTICS:								
<b>45</b>		(ii) (ii)	(A) LENGTH: 105 (B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single (D) TOPOLOGY: Linear KIND: cDNA to genomic RNA KIND (if peptide or protein): (A) SEQUENCE ASSEMBLY METHOD: Overlap (B) FRAGMENT TYPE: Internal Fragment								

					(C)		HYP	THE:	l I CA I	<b>:</b> _						
	(iii)			ORIGINAL SOURCE: HIV												
				•		(E) INDIVIDUAL ISOLATE:										
5	(iv	)		EDIA		OURCI	Z:									
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			(v)						ME:					^~~	· ····································	
			(vi)		PROPERTIES OF SEQUENCE: Expresses cantigenic d											
10			(vi	ii)	SEQUENCE DESCRIPTION:											
	SEQ ID NO: EE					636–2										
15																
	1				5					10					15	
		Thr	Aro	Pro		Agn	Asn	Thr	Arg		Ser	Ile	His	Ile	G1y	
	TGT	ACA	AGA	CCC	AAC	AAC	AAT	ACA	AGA	AAA	AGT	ATA	CAT	ATA	GGA	
20																
					20					25					30	
	Pro	G1 v	Arg	A1a	Phe	Tvr	Thr	Thr	G1v	Glu	Ile	Ile	G1y	Asn	Ile	
	CCA	GGG	AGA	GCA	TTT	TAT	ACA	ACA	GGA	GAA	ATA	ATA	GGA	AAT	ATA	
25																
					35											
	Arg	Gln	Ala	His	Cys											
				CAT												
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30																
	(2)						-		NO: 1							
			(i)		SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 (B) TYPE: Nucleic Acid											
					(B)											
35					(C)				DNES		Sing	те				
				`	(D)	<b>.</b> .			Y: :							
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40					(A) (B)		-		T TY					agme.	-	
					(c)				TICA		1110	C. I.a		a6mc		
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45			114	•	(C)		CLO									
			(v)			ITIO			OME:	Wit	hin	Env	Gene	<del></del>		
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SEQ ID NO: EE6636-3

1 5 10 15

Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly
TGT ACA AGA CCC AAC AAC AAT ACA AGA AAA AGT ATA CAT ATA GGA

20 25 30
Pro Gly Arg Ala Phe Tyr Thr Thr Gly Glu Ile Ile Gly Asn Ile
CCA GGG AGA GCA TTT TAT ACA ACA GGA GAA ATA ATA GGA AAT ATA

35 Arg Gln Ala His Cys AGA CAA GCA CAT TGT

Claims

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 An antigenic conjugate of HIV major neutralization determinant covalently linked to purified outer membrane proteosome of Neisseria, comprising an antigenic conjugate of the formula

(PND)<sub>n</sub>~(Omp),

or pharmaceutically acceptable salt thereof, wherein:

PND is the major neutralization determinant of HIV, which is a polypeptide of one or more amino acid sequences;

n indicates the number of polypeptides of PND covalently linked to Omp and is 1-50;

indicates covalent linkage;

Omp is purified outer membrane proteosome of Neisseria,

said polypeptide having a sequence of 35 amino acids or less, but at least 5 amino acids in length; said polypeptide containing in its sequence Gly-X-Gly, wherein X is proline, leucine, alanine, glutamine or serine;

said polypeptide having any of the sequences given in the sequence listing with the exception of sequence nos. EE90-1, EE90-2, EE90-3, EE312-1, EE360-1, EE360-2, EE360-3, EE667-3 and EE6405-3

2. The antigenic conjugate of claim 1 wherein X is proline.

- The antigenic conjugate of claim 1 wherein the covalent linkage between PND and Omp consists essentially of a bigeneric spacer.
- The antigenic conjugate of claims 1-3, in combination with any of the antivirals, immunomodulators, anti-infectives or vaccines of Table I.
  - 5. The antigenic conjugate of claims 1-3, wherein said Omp is derived from Neisseria meningitidis.
  - 6. A cocktail of antigenic conjugates consisting essentially of a mixture of more than one molecular species of the antigenic conjugates of claims 1-3.
- An AIDS vaccine comprising an antigenic conjugate of HIV major neutralization determinant covalently
   linked to purified outer membrane proteosome of Neisseria, said conjugate of the formula

(PND)<sub>n</sub>~(Omp),

or pharmaceutically acceptable salt thereof, wherein:

PND is the major neutralization determinant of HIV, which is a polypeptide of one or more amino acid sequences;

- n indicates the number of polypeptides of PND covalently linked to Omp and is 1-50;
- indicates covalent linkage;

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Omp is purified outer membrane proteosome of Neisseria;

said polypeptide having a sequence of 35 amino acids or less, but at least 5 amino acids in length; said polypeptide containing in its sequence Gly-X-Gly, wherein X is proline, leucine, alanine, glutamine or serine;

said polypeptide having any of the sequences given in the sequence listing;

said conjugate mixed with a suitable immunological adjuvant, carrier or vector, said vaccine to be used pre- and post-exposure to prevent or treat HIV infection or disease, said vaccine capable of eliciting specific HIV neutralizing antibodies.

- 15 8. The AIDS vaccine of claim 7 wherein X is proline.
  - The AIDS vaccine of claim 7 wherein the covalent linkage betwen PND and Omp consists essentially of a bigeneric spacer.
- 20 10. The AIDS vaccine of claims 7-9 in combination with any of the antivirals, immunomodulators, anti-infectives or vaccines of Table I.
  - 11. The AIDS vaccine of claims 7-9, wherein said Omp is derived from Neisseria meningitidis.
- 12. The AIDS vaccine of claism 7-9 comprising a cocktail of said antigenic conjugates, said cocktail consisting essentially of a mixture of more than one molecular species of said antigenic conjugates.
  - 13. A pharmaceutical composition comprising an antigenic conjugate of HIV major neutralization determinant covalently linked to purified outer membrane proteosome of Neisseria, said antigenic conjugate of the formula

(PND)n~(Omp),

or pharmaceutically acceptable salt thereof, wherein:

PND is the major neutralization determinant of HIV, which is a polypeptide of one or more amino acid sequences:

- n indicates the number of polupeptides of PND covalently linked to Omp and is 1-50;
- ~ indicates covalent linkage;

Omp is purified outer membrane proteosome of Neisseria,

said polypeptide having a sequence of 35 amino acids or less, but at least 5 amino acids in length; said polypeptide containing in its sequence Gly-X-Gly, wherein X is proline, leucine, alanine, glutamine or serine;

said polypeptide having any of the sequences given in the sequence listing;

said conjugate mixed with a suitable immunological adjuvant, said composition useful as a vaccine capable of producing specific HIV neutralizing antibody in mammals.

- 14. The composition of claim 13 wherein X is proline.
- 15. The composition of claim 13 wherein the covalent linkage between PND and Omp consists essentiallyof a bigeneric spacer.
  - 16. The composition of claims 13-15, in combination with any of the antivirals, immunomodulators, antiinfectives or vaccines of Table I.
- 17. The composition of claims 13-15, wherein said Omp is derived from Neisseria meningitidis.
  - 18. A pharmaceutical composition containing a cocktail of antigenic conjugates consisting essentially of a mixture of more than one molecular species of the antigenic conjugates of claims 13-15.

- 19. The use of a conjugate as claimed in claim 1 for the preparation of a medicament for vaccinating against AIDS or ARC.
- 20. The use of a conjugate as claimed in claim 2 for the preparation of a medicament for vaccinating against AIDS or ARC.
  - 21. The use of a conjugate as claimed in claim 3 for the preparation of a medicament for vaccinating against AIDS or ARC.
- 22. The use of a conjugate as claimed in claim 1 together with any of the antivirals, immunolodulators or anti-infectives of Table I for the preparation of a medicament for vaccinating against AIDS or ARC.
  - 23. The use as claimed in claim 19 or 20 wherein the Omp is derived from Neisseria meningitidis.
- 24. The use of a conjugate as claimed in claim 1 for the preparation of a medicament for the prevention or treatment of infection by HIV, or for the treatment of AIDS.
  - 25. The use of a conjugate as claimed in claim 2 for the preparation of a medicament for the prevention or treatment of infection by HIV, or for the treatment of AIDS.
  - 26. The use of a conjugate as claimed in claim 3 for the preparation of a medicament for the prevention or treatment of infection by HIV, or for the treatment of AIDS.
- 27. The use of a conjugate as claimed in claim 1 together with any of the antivirals, immunolodulators or anti-infectives of Table I for the preparation of a medicament for the prevention or treatment of infection by HIV, or for the treatment of AIDS.
  - 28. The use as claimed in claim 24 or 25 wherein the Omp is derived from Neisseria meningitidis.

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